GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 26, 2006, 02:37:44 ; Search time 47 Seconds
(without alignments)
156.556 Million cell updates/sec

Title: US-10-785-230-5
Perfect score: 463
Sequence: 1 MNAKVVVVLVLVLTALCLSD.....VCIDPKLKWIQEYLEKALNK 89

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	463	100.0	89	1	US-08-323-084A-1	Sequence 1, Appli
2	463	100.0	89	1	US-08-674-008-1	Sequence 1, Appli
3	463	100.0	89	2	US-09-461-912A-46	Sequence 46, Appl
4	463	100.0	89	2	US-09-175-713-1	Sequence 1, Appli
5	463	100.0	89	2	US-09-647-501-4	Sequence 4, Appli
6	463	100.0	93	1	US-08-323-084A-5	Sequence 5, Appli
7	463	100.0	93	1	US-08-674-008-5	Sequence 5, Appli
8	463	100.0	93	2	US-09-919-497-95	Sequence 95, Appl
9	463	100.0	93	2	US-09-949-016-5967	Sequence 5967, Ap
10	463	100.0	93	2	US-09-144-838-7	Sequence 7, Appli
11	463	100.0	93	2	US-09-175-713-2	Sequence 2, Appli

12	463	100.0	119	2	US-09-949-016-8247	Sequence 8247, Ap
13	463	100.0	166	2	US-09-646-028-5	Sequence 5, Appli
14	463	100.0	328	2	US-08-808-720-1	Sequence 1, Appli
15	463	100.0	328	2	US-09-467-638-1	Sequence 1, Appli
16	442	95.5	89	1	US-08-181-556-2	Sequence 2, Appli
17	442	95.5	93	2	US-09-312-283C-421	Sequence 421, App
18	440	95.0	326	2	US-08-808-720-3	Sequence 3, Appli
19	440	95.0	326	2	US-09-467-638-3	Sequence 3, Appli
20	377	81.4	177	2	US-09-646-028-54	Sequence 54, Appl
21	377	81.4	339	2	US-09-646-028-55	Sequence 55, Appl
22	369	79.7	90	2	US-09-175-713-12	Sequence 12, Appl
23	369	79.7	94	2	US-09-175-713-13	Sequence 13, Appl
24	365	78.8	68	2	US-09-175-713-14	Sequence 14, Appl
25	365	78.8	69	2	US-09-175-713-10	Sequence 10, Appl
26	365	78.8	72	2	US-09-175-713-15	Sequence 15, Appl
27	365	78.8	72	2	US-09-646-193-7	Sequence 7, Appli
28	365	78.8	72	2	US-09-646-192-7	Sequence 7, Appli
29	365	78.8	73	2	US-09-175-713-11	Sequence 11, Appl
30	360	77.8	67	2	US-09-144-838-8	Sequence 8, Appli
31	360	77.8	67	2	US-09-144-838-23	Sequence 23, Appl
32	360	77.8	67	2	US-09-646-193-6	Sequence 6, Appli
33	360	77.8	67	2	US-09-646-192-6	Sequence 6, Appli
34	342.5	74.0	66	2	US-09-144-838-27	Sequence 27, Appl
35	321	69.3	68	2	US-09-144-838-51	Sequence 51, Appl
36	309	66.7	68	2	US-09-144-838-24	Sequence 24, Appl
37	306	66.1	67	2	US-09-144-838-25	Sequence 25, Appl
38	304	65.7	67	2	US-09-144-838-47	Sequence 47, Appl
39	291.5	63.0	67	2	US-09-144-838-28	Sequence 28, Appl
40	270	58.3	69	2	US-09-144-838-52	Sequence 52, Appl
41	268.5	58.0	66	2	US-09-144-838-29	Sequence 29, Appl
42	267	57.7	68	2	US-09-144-838-53	Sequence 53, Appl
43	255	55.1	68	2	US-09-144-838-26	Sequence 26, Appl
44	253	54.6	68	2	US-09-144-838-48	Sequence 48, Appl
45	250	54.0	67	2	US-09-144-838-49	Sequence 49, Appl

ALIGNMENTS

```
RESULT 1
US-08-323-084A-1
; Sequence 1, Application US/08323084A
; Patent No. 5563048
;  GENERAL INFORMATION:
;    APPLICANT:  HONJO, TASUKU
;    APPLICANT:  SHIROZU, MICHIO
;    APPLICANT:  TADA, HIDEAKI
;    TITLE OF INVENTION:  No. 5563048el Polypeptides and DNAs encoding them
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SUGHRUE, MION, ZINN, MACPEAK & SEAS
;      STREET:  2100 Pennsylvania Avenue, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20037-3202
;    COMPUTER READABLE FORM:
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;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/323,084A
;       FILING DATE:
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 280505/1993
;       FILING DATE:  14-OCT-1993
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202)293-7060
;       TELEFAX:  (202)293-7860
;       TELEX:  6491103
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  89 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-323-084A-1

  Query Match             100.0%;  Score 463;  DB 1;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 9.8e-52;
  Matches   89;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

Qy         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
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Db         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89


RESULT 2
US-08-674-008-1
; Sequence 1, Application US/08674008
; Patent No. 5756084
;  GENERAL INFORMATION:
;    APPLICANT:  HONJO, Tasuku
;    APPLICANT:  SHIROZU, Michio
;    APPLICANT:  TADA, Hideaki
;    TITLE OF INVENTION:  HUMAN STROMAL DERIVED
;    TITLE OF INVENTION:  FACTOR 1` AND 1  (As Amended)
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SUGHRUE, MION, ZINN, MACPEAK & SEAS
;      STREET:  2100 Pennsylvania Avenue, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20037-3202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
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;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/674,008
;       FILING DATE:  1-JUL-1996
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/323,084
;       FILING DATE:  14-OCT-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 280505/1993
;       FILING DATE:  14-OCT-1993
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202)293-7060
;       TELEFAX:  (202)293-7860
;       TELEX:  6491103
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  89 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-674-008-1

  Query Match             100.0%;  Score 463;  DB 1;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 9.8e-52;
  Matches   89;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
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Db          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

Qy         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
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Db         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89


RESULT 3
US-09-461-912A-46
; Sequence 46, Application US/09461912A
; Patent No. 6709855
; GENERAL INFORMATION:
;  APPLICANT:  Stanton, Lawrence A.
;  APPLICANT:  White, R. Tyler
;  APPLICANT:  Damm, Deborah L.
;  APPLICANT:  Lewicki, John A.
;  TITLE OF INVENTION:  Methods for detection and use of
;  TITLE OF INVENTION:  differentially expressed genes in disease states
;  FILE REFERENCE:  SCIOS.011A
;  CURRENT APPLICATION NUMBER: US/09/461,912A
;  CURRENT FILING DATE:  1999-12-15
;  PRIOR APPLICATION NUMBER:  US 60/113,008
;  PRIOR FILING DATE:  1998-12-18
;  NUMBER OF SEQ ID NOS:  48
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 46
;   LENGTH: 89
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;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-461-912A-46

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  Best Local Similarity   100.0%;  Pred. No. 9.8e-52;
  Matches   89;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
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Db          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

Qy         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
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Db         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89


RESULT 4
US-09-175-713-1
; Sequence 1, Application US/09175713
; Patent No. 6852508
;  GENERAL INFORMATION:
;    APPLICANT:  Herrmann, Stephen H.
;    APPLICANT:  Lu, Zhijian
;    APPLICANT:  McCoy, John M.
;    APPLICANT:  Swanberg, Stephen L.
;    APPLICANT:  Walker, Bruce
;    APPLICANT:  Yang, Otto
;    TITLE OF INVENTION:  CHEMOKINES WITH AMINO-TERMINAL MODIFICATIONS
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc.
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  U.S.A.
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/175,713
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sprunger, Suzanne A.
;      REGISTRATION NUMBER:  41,323
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 498-8284
;      TELEFAX:  (617) 876-5851
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  89 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
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;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-175-713-1

  Query Match             100.0%;  Score 463;  DB 2;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 9.8e-52;
  Matches   89;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

Qy         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
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Db         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89


RESULT 5
US-09-647-501-4
; Sequence 4, Application US/09647501
; Patent No. 6863887
; GENERAL INFORMATION:
;  APPLICANT: No. 6863887thwest Biotherapeutics, Inc.
;  APPLICANT:  Murphy, Gerald P.
;  APPLICANT:  Boynton, Alton L.
;  APPLICANT:  Sehgal, Anil
;  TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC APPLICATIONS BASED ON THE
;  TITLE OF INVENTION:  ROLE OF THE CXCR-4 GENE IN TUMORIGENESIS
;  FILE REFERENCE: 20093-000600PC
;  CURRENT APPLICATION NUMBER: US/09/647,501
;  CURRENT FILING DATE:  2000-09-24
;  PRIOR APPLICATION NUMBER: 60/079,916
;  PRIOR FILING DATE: 1998-03-30
;  PRIOR APPLICATION NUMBER: 60/104,656
;  PRIOR FILING DATE: 1998-10-16
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 89
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-647-501-4

  Query Match             100.0%;  Score 463;  DB 2;  Length 89;
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  Matches   89;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
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Db          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

Qy         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
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Db         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89


RESULT 6
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US-08-323-084A-5
; Sequence 5, Application US/08323084A
; Patent No. 5563048
; GENERAL INFORMATION:
; APPLICANT: HONJO, TASUKU
; APPLICANT: SHIROZU, MICHIO
; APPLICANT: TADA, HIDEAKI
; TITLE OF INVENTION: No. 5563048el Polypeptides and DNAs encoding them
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/323,084A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 280505/1993
; FILING DATE: 14-OCT-1993
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 93 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-323-084A-5

Query Match 100.0%; Score 463; DB 1; Length 93;
Best Local Similarity 100.0%; Pred. No. 1e-51;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

Qy         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
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Db         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
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RESULT 7
US-08-674-008-5
; Sequence 5, Application US/08674008
; Patent No. 5756084

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;  GENERAL INFORMATION:
;    APPLICANT:  HONJO, Tasuku
;    APPLICANT:  SHIROZU, Michio
;    APPLICANT:  TADA, Hideaki
;    TITLE OF INVENTION:  HUMAN STROMAL DERIVED
;    TITLE OF INVENTION:  FACTOR 1` AND 1  (As Amended)
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SUGHRUE, MION, ZINN, MACPEAK & SEAS
;      STREET:  2100 Pennsylvania Avenue, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20037-3202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/674,008
;      FILING DATE:  1-JUL-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/323,084
;      FILING DATE:  14-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 280505/1993
;      FILING DATE:  14-OCT-1993
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)293-7060
;      TELEFAX:  (202)293-7860
;      TELEX:  6491103
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  93 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-674-008-5

  Query Match             100.0%;  Score 463;  DB 1;  Length 93;
  Best Local Similarity   100.0%;  Pred. No. 1e-51;
  Matches   89;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
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Db         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89


RESULT 8
US-09-919-497-95
; Sequence 95, Application US/09919497
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; Patent No. 6773883
; GENERAL INFORMATION:
; APPLICANT: Mutter, George L.
; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
; FILE REFERENCE: B0801/7225
; CURRENT APPLICATION NUMBER: US/09/919,497
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/221,735
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 95
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-919-497-95

Query Match 100.0%; Score 463; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 1e-51;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
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Db         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
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RESULT 9
US-09-949-016-5967
; Sequence 5967, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5967
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-5967

Query Match 100.0%; Score 463; DB 2; Length 93;

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  Best Local Similarity   100.0%;  Pred. No. 1e-51;
  Matches   89;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
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Qy         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
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Db         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89


RESULT 10
US-09-144-838-7
; Sequence 7, Application US/09144838A
; Patent No. 6844161
; GENERAL INFORMATION:
;  APPLICANT: Siani, Michael A.
;  APPLICANT: Wilken, Jill
;  APPLICANT: Simon, Reyna
;  APPLICANT: Kent, Stephen B.H.
;  TITLE OF INVENTION: Modular Protein Libraries and Methods of Preparation
;  FILE REFERENCE: GRFN-020/01US
;  CURRENT APPLICATION NUMBER: US/09/144,838A
;  CURRENT FILING DATE: 1998-08-31
;  EARLIER APPLICATION NUMBER: US 60/057,620
;  EARLIER FILING DATE: 1997-09-04
;  NUMBER OF SEQ ID NOS: 54
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 93
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-144-838-7

  Query Match             100.0%;  Score 463;  DB 2;  Length 93;
  Best Local Similarity   100.0%;  Pred. No. 1e-51;
  Matches   89;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
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Db          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

Qy         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
              |||||||||||||||||||||||||||||
Db         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89


RESULT 11
US-09-175-713-2
; Sequence 2, Application US/09175713
; Patent No. 6852508
;  GENERAL INFORMATION:
;    APPLICANT:  Herrmann, Stephen H.
;    APPLICANT:  Lu, Zhijian
```

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;    APPLICANT:  McCoy, John M.
;    APPLICANT:  Swanberg, Stephen L.
;    APPLICANT:  Walker, Bruce
;    APPLICANT:  Yang, Otto
;    TITLE OF INVENTION:  CHEMOKINES WITH AMINO-TERMINAL MODIFICATIONS
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc.
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  U.S.A.
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/175,713
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sprunger, Suzanne A.
;      REGISTRATION NUMBER:  41,323
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 498-8284
;      TELEFAX:  (617) 876-5851
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  93 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-175-713-2

  Query Match             100.0%;  Score 463;  DB 2;  Length 93;
  Best Local Similarity   100.0%;  Pred. No. 1e-51;
  Matches   89;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

Qy         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
              |||||||||||||||||||||||||||||
Db         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89


RESULT 12
US-09-949-016-8247
; Sequence 8247, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
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; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8247
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8247

Query Match 100.0%; Score 463; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.4e-51;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
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Db         27 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 86

Qy         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
              |||||||||||||||||||||||||||||
Db         87 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 115
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RESULT 13
US-09-646-028-5
; Sequence 5, Application US/09646028
; Patent No. 6562347
; GENERAL INFORMATION:
; APPLICANT: Kwak, Larry
; APPLICANT: Biragyn, Arya
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
; TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES
; FILE REFERENCE: 14014.0316/P
; CURRENT APPLICATION NUMBER: US/09/646,028
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/077,745
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-09-646-028-5

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  Query Match             100.0%;  Score 463;  DB 2;  Length 166;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-51;
  Matches   89;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

Qy         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
              |||||||||||||||||||||||||||||
Db         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89


RESULT 14
US-08-808-720-1
; Sequence 1, Application US/08808720
; Patent No. 6100387
;  GENERAL INFORMATION:
;    APPLICANT:  Herrmann, Steve
;    APPLICANT:  Swanberg, Stephen
;    TITLE OF INVENTION:  CHIMERIC POLYPEPTIDES CONTAINING
;    TITLE OF INVENTION:  CHEMOKINE DOMAINS
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Insititute, Inc.
;      STREET:  87 CambridgePark
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/808,720
;      FILING DATE:
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sprunger, Suzanne
;      REGISTRATION NUMBER:  P-41,323
;      REFERENCE/DOCKET NUMBER:  GI5291
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 498-8284
;      TELEFAX:  (617) 876-5851
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  328 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-808-720-1

  Query Match             100.0%;  Score 463;  DB 2;  Length 328;
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  Best Local Similarity   100.0%;  Pred. No. 5.1e-51;
  Matches   89;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

Qy         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
              |||||||||||||||||||||||||||||
Db         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89


RESULT 15
US-09-467-638-1
; Sequence 1, Application US/09467638
; Patent No. 6730296
;  GENERAL INFORMATION:
;    APPLICANT:  Herrmann, Steve
;    APPLICANT:  Swanberg, Stephen
;    TITLE OF INVENTION:  CHIMERIC POLYPEPTIDES CONTAINING
;    TITLE OF INVENTION:  CHEMOKINE DOMAINS
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Insititute, Inc.
;      STREET:  87 CambridgePark
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/467,638
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/808,720
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sprunger, Suzanne
;      REGISTRATION NUMBER:  P-41,323
;      REFERENCE/DOCKET NUMBER:  GI5291
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 498-8284
;      TELEFAX:  (617) 876-5851
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  328 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-467-638-1
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Query Match 100.0%; Score 463; DB 2; Length 328;
Best Local Similarity 100.0%; Pred. No. 5.1e-51;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

Qy         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
              |||||||||||||||||||||||||||||
Db         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
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Search completed: April 26, 2006, 02:39:05
Job time : 47 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 26, 2006, 02:30:38 ; Search time 225 Seconds
(without alignments)
279.076 Million cell updates/sec

Title: US-10-785-230-5
Perfect score: 463
Sequence: 1 MNAKVVVVLVLVLTALCLSD.....VCIDPKLKWIQEYLEKALNK 89

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	463	100.0	89	2	Q6ICW0_HUMAN	Q6icw0 homo sapien
2	463	100.0	92	2	Q9H554_HUMAN	Q9h554 homo sapien
3	463	100.0	93	1	SDF1_HUMAN	P48061 homo sapien
4	463	100.0	119	2	Q5IT36_HUMAN	Q5it36 homo sapien
5	455	98.3	89	2	Q8HYP0_MACMU	Q8hyp0 macaca mula
6	447	96.5	93	2	Q5R8M6_PONPY	Q5r8m6 pongo pygma
7	445	96.1	89	2	Q54AJ3_FELCA	Q54aj3 felis silve
8	445	96.1	93	1	SDF1_FELCA	O62657 felis silve
9	442	95.5	89	1	SDF1_MOUSE	P40224 mus musculu
10	442	95.5	89	2	Q543V6_MOUSE	Q543v6 mus musculu
11	442	95.5	93	2	Q4FJL5_MOUSE	Q4fjl5 mus musculu
12	442	95.5	137	2	Q80ZW4_MOUSE	Q80zw4 mus musculu
13	437	94.4	89	2	Q5XNN9_CANFA	Q5xnn9 canis famil
14	435	94.0	89	2	Q9QZD1_RAT	Q9qzd1 rattus norv
15	435	94.0	119	2	Q80YV8_RAT	Q80yv8 rattus norv

16	428	92.4	116	2	Q6EKW4_PIG	Q6ekw4 sus scrofa
17	359	77.5	89	2	Q6T7C0_CHICK	Q6t7c0 gallus gall
18	359	77.5	131	2	Q6T7B9_CHICK	Q6t7b9 gallus gall
19	341	73.7	93	2	Q5EBF6_XENTR	Q5ebf6 xenopus tro
20	341	73.7	94	2	Q8UUJ9_XENLA	Q8uuj9 xenopus lae
21	225.5	48.7	99	2	Q4QTK3_ICTPU	Q4qtk3 ictalurus p
22	224.5	48.5	99	2	Q8AV10_BRARE	Q8av10 brachydanio
23	220.5	47.6	97	2	Q6V9B5_BRARE	Q6v9b5 brachydanio
24	209.5	45.2	97	2	Q70V43_CYPCA	Q70v43 cyprinus ca
25	207.5	44.8	98	2	Q4RQF0_TETNG	Q4rqf0 tetraodon n
26	206.5	44.6	99	2	Q5ZP81_CYPCA	Q5zp81 cyprinus ca
27	122	26.3	98	2	Q8QGV8_PAROL	Q8qgv8 paralichthy
28	122	26.3	109	2	Q90Y59_PAROL	Q90y59 paralichthy
29	116	25.1	101	1	IL8_FELCA	Q9xsx5 felis silve
30	113.5	24.5	101	1	IL8_CAVPO	P49113 cavia porce
31	113	24.4	97	2	Q6LAE6_HUMAN	Q6lae6 homo sapien
32	113	24.4	99	1	IL8_HUMAN	P10145 h interleuk
33	113	24.4	99	2	Q6FGF6_HUMAN	Q6fgf6 homo sapien
34	112.5	24.3	96	1	GROA_MOUSE	P12850 mus musculu
35	112.5	24.3	107	2	Q5U5W9_MOUSE	Q5u5w9 mus musculu
36	111.5	24.1	107	2	Q6PUD4_PIG	Q6pud4 sus scrofa
37	111	24.0	98	1	SCYBA_RAT	P48973 rattus norv
38	111	24.0	101	1	IL8_CANFA	P41324 canis famil
39	110.5	23.9	107	2	Q6PUJ1_PIG	Q6puj1 sus scrofa
40	110	23.8	103	1	IL8_CHICK	P08317 gallus gall
41	109.5	23.7	42	2	Q75PL0_ORYLA	Q75pl0 oryzias lat
42	109.5	23.7	91	1	CCL5_SIGHI	Q91zl1 sigmodon hi
43	109	23.5	98	2	Q6GTC7_RAT	Q6gtc7 rattus norv
44	108.5	23.4	91	1	CCL5_MACMU	Q8hyq1 macaca mula
45	107	23.1	101	1	IL8_MACMU	P67813 macaca mula

ALIGNMENTS

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RESULT 1
Q6ICW0_HUMAN
ID   Q6ICW0_HUMAN PRELIMINARY;      PRT;    89 AA.
AC   Q6ICW0;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   CXCL12 protein (Stromal cell-derived factor 1a) (Fragment).
GN   Name=CXCL12;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
RL   Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Zhao X., Zhang H., Lee S., Wong K., Zheng B.;
RT   "Polymorphism study of cell-derived factor 1 (SDF1) gene and their
```

```
RT   correlation with HIV infection in a Chinese cohort.";
RL   Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; CR450283; CAG29279.1; -; mRNA.
DR   EMBL; AY874118; AAW82036.1; -; mRNA.
FT   NON_TER      89     89
SQ   SEQUENCE   89 AA;  10103 MW;  62B44E8D209C3A14 CRC64;

  Query Match             100.0%;  Score 463;  DB 2;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 6.2e-44;
  Matches   89;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

Qy         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
              |||||||||||||||||||||||||||||
Db         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89


RESULT 2
Q9H554_HUMAN
ID   Q9H554_HUMAN PRELIMINARY;      PRT;    92 AA.
AC   Q9H554;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Chemokine (C-X-C motif) ligand 12 (Stromal cell-derived factor
DE   1).
GN   Name=CXCL12; ORFNames=RP11-20J15.4-002;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Bird C.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL137026; CAC10202.1; -; Genomic_DNA.
DR   HSSP; P48061; 1SDF.
DR   SMR; Q9H554; 23-88.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0008009; F:chemokine activity; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR002473; C-X-C/Interlkn_8.
DR   InterPro; IPR001811; Chemokine_IL8.
DR   Pfam; PF00048; IL8; 1.
DR   PRINTS; PR00436; INTERLEUKIN8.
DR   SMART; SM00199; SCY; 1.
SQ   SEQUENCE   92 AA;  10510 MW;  AEF0C402B44E8D20 CRC64;

  Query Match             100.0%;  Score 463;  DB 2;  Length 92;
  Best Local Similarity   100.0%;  Pred. No. 6.4e-44;
  Matches   89;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
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Db            1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

Qy           61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
                ||||||||||||||||||||||||||||
Db           61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89


RESULT 3
SDF1_HUMAN
ID   SDF1_HUMAN     STANDARD;      PRT;    93 AA.
AC   P48061;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Stromal cell-derived factor 1 precursor (SDF-1) (CXCL12) (Pre-B cell
DE   growth stimulating factor) (PBSF) (hIRH) [Contains: SDF-1-beta(3-72);
DE   SDF-1-alpha(3-67)].
GN   Name=CXCL12; Synonyms=SDF1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Spotila L.D.;
RL   Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=96039262; PubMed=7490086;
RA   Shirozu M., Nakano T., Inazawa J., Tashiro K., Tada H., Shinohara T.,
RA   Honjo T.;
RT   "Structure and chromosomal localization of the human stromal cell-
RT   derived factor 1 (SDF1) gene.";
RL   Genomics 28:495-500(1995).
RN   [3]
RP   NUCLEOTIDE SEQUENCE (ISOFORM ALPHA).
RC   TISSUE=Liver;
RA   Begum N.A., Barnard G.F.;
RT   "Nucleotide sequence of hIRH, human intercrine reduced in hepatomas.";
RL   Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA   Rieder M.J., Johanson E.J., da Ponte S.H., Hastings N.C., Ahearn M.O.,
RA   Bertucci C.B., Wong M.W., Yi Q., Nickerson D.A.;
RT   "SeattleSNPs. NHLBI HL66682 program for genomic applications, UW-
RT   FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL   Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   PubMed=15164054; DOI=10.1038/nature02462;
RA   Deloukas P., Earthrowl M.E., Grafham D.V., Rubenfield M., French L.,
RA   Steward C.A., Sims S.K., Jones M.C., Searle S., Scott C., Howe K.,
RA   Hunt S.E., Andrews T.D., Gilbert J.G.R., Swarbreck D., Ashurst J.L.,
RA   Taylor A., Battles J., Bird C.P., Ainscough R., Almeida J.P.,
RA   Ashwell R.I.S., Ambrose K.D., Babbage A.K., Bagguley C.L., Bailey J.,
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RA Banerjee R., Bates K., Beasley H., Bray-Allen S., Brown A.J.,
RA Brown J.Y., Burford D.C., Burrill W., Burton J., Cahill P., Camire D.,
RA Carter N.P., Chapman J.C., Clark S.Y., Clarke G., Clee C.M., Clegg S.,
RA Corby N., Coulson A., Dhami P., Dutta I., Dunn M., Faulkner L.,
RA Frankish A., Frankland J.A., Garner P., Garnett J., Gribble S.,
RA Griffiths C., Grocock R., Gustafson E., Hammond S., Harley J.L.,
RA Hart E., Heath P.D., Ho T.P., Hopkins B., Horne J., Howden P.J.,
RA Huckle E., Hynds C., Johnson C., Johnson D., Kana A., Kay M.,
RA Kimberley A.M., Kershaw J.K., Kokkinaki M., Laird G.K., Lawlor S.,
RA Lee H.M., Leongamornlert D.A., Laird G., Lloyd C., Lloyd D.M.,
RA Loveland J., Lovell J., McLaren S., McLay K.E., McMurray A.,
RA Mashreghi-Mohammadi M., Matthews L., Milne S., Nickerson T.,
RA Nguyen M., Overton-Larty E., Palmer S.A., Pearce A.V., Peck A.I.,
RA Pelan S., Phillimore B., Porter K., Rice C.M., Rogosin A., Ross M.T.,
RA Sarafidou T., Sehra H.K., Shownkeen R., Skuce C.D., Smith M.,
RA Standring L., Sycamore N., Tester J., Thorpe A., Torcasso W.,
RA Tracey A., Tromans A., Tsolas J., Wall M., Walsh J., Wang H.,
RA Weinstock K., West A.P., Willey D.L., Whitehead S.L., Wilming L.,
RA Wray P.W., Young L., Chen Y., Lovering R.C., Moschonas N.K.,
RA Siebert R., Fechtel K., Bentley D., Durbin R., Hubbard T.,
RA Doucette-Stamm L., Beck S., Smith D.R., Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 10.";
RL Nature 429:375-381(2004).
RN [6]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM ALPHA).
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [7]
RP IDENTIFICATION OF SDF-1ALPHA(3-67) AND SDF-1BETA(3-72) BY MASS
RP SPECTROMETRY, AND N-TERMINAL AND C-TERMINAL PROCESSING.
RX PubMed=14525775; DOI=10.1182/blood-2003-08-2857;
RA De La Luz Sierra M., Yang F., Narazaki M., Salvucci O., Davis D.,
RA Yarchoan R., Zhang H.H., Fales H., Tosato G.;
RT "Differential processing of stromal-derived factor-1alpha and beta
RT explains functional diversity.";
RL Blood 103:2452-2459(2004).
RN [8]

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RP   STRUCTURE BY NMR OF 22-88.
RX   MEDLINE=98046030; PubMed=9384579; DOI=10.1093/emboj/16.23.6996;
RA   Crump M.P., Gong J.H., Loetscher P., Rajarathnam K., Amara A.,
RA   Arenzana-Seisdedos F., Virelizier J.L., Baggiolini M., Sykes B.D.,
RA   Clark-Lewis I.;
RT   "Solution structure and basis for functional activity of stromal cell-
RT   derived factor-1; dissociation of CXCR4 activation from binding and
RT   inhibition of HIV-1.";
RL   EMBO J. 16:6996-7007(1997).
RN   [9]
RP   X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 22-88.
RX   MEDLINE=98284037; PubMed=9618518; DOI=10.1073/pnas.95.12.6941;
RA   Dealwis C., Fernandez E.J., Thompson D.A., Simon R.J., Siani M.A.,
RA   Lolis E.;
RT   "Crystal structure of chemically synthesized [N33A] stromal cell-
RT   derived factor 1alpha, a potent ligand for the HIV-1 'fusin'
RT   coreceptor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 95:6941-6946(1998).
CC   -!- FUNCTION: Chemoattractant active on T-lymphocytes, monocytes, but
CC       not neutrophils. SDF-1-beta(3-72) and SDF-1-alpha(3-67) show a
CC       reduced chemotactic activity. Binding to cell surface
CC       proteoglycans seems to inhibit formation of SDF-1-alpha(3-67) and
CC       thus to preserve activity on local sites.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=Beta; Synonyms=SDF-1-beta(1-72);
CC         IsoId=P48061-1; Sequence=Displayed;
CC       Name=Alpha; Synonyms=SDF-1-alpha(1-68);
CC         IsoId=P48061-2; Sequence=VSP_001056;
CC   -!- PTM: Processed forms SDF-1-beta(3-72) and SDF-1-alpha(3-67) are
CC       produced after secretion by proteolytic cleavage of isoforms Beta
CC       and Alpha, respectively. The N-terminal processing is probably
CC       achieved by DPP4. Isoform Alpha is first cleaved at the C-terminus
CC       to yield a SDF-1-alpha(1-67) intermediate before being processsed
CC       at the N-terminus. The C-terminal processing of isoform Alpha is
CC       reduced by binding to heparin and, probably, cell surface
CC       proteoglycans.
CC   -!- SIMILARITY: Belongs to the intercrine alpha (chemokine CxC)
CC       family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; U16752; AAA97434.1; -; mRNA.
DR   EMBL; L36033; AAB39332.1; -; mRNA.
DR   EMBL; L36034; AAB39333.1; -; mRNA.
DR   EMBL; U19495; AAB40516.1; -; mRNA.
DR   EMBL; AY802782; AAV49999.1; -; Genomic_DNA.
DR   EMBL; AL137026; CAC10203.1; -; Genomic_DNA.
DR   EMBL; BC039893; AAH39893.1; -; mRNA.
DR   PIR; G01540; G01540.
DR   PDB; 1A15; X-ray; A/B=22-88.
DR   PDB; 1QG7; X-ray; A/B=22-88.
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DR   PDB; 1SDF; NMR; @=22-88.
DR   PDB; 1VMC; NMR; A=20-89.
DR   PDB; 2SDF; NMR; @=22-88.
DR   Ensembl; ENSG00000107562; Homo sapiens.
DR   HGNC; HGNC:10672; CXCL12.
DR   MIM; 600835; -.
DR   GO; GO:0008009; F:chemokine activity; TAS.
DR   GO; GO:0005102; F:receptor binding; TAS.
DR   GO; GO:0006874; P:calcium ion homeostasis; TAS.
DR   GO; GO:0007155; P:cell adhesion; TAS.
DR   GO; GO:0006935; P:chemotaxis; TAS.
DR   GO; GO:0008015; P:circulation; TAS.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
DR   GO; GO:0006955; P:immune response; TAS.
DR   GO; GO:0008064; P:regulation of actin polymerization and/or d. . .; TAS.
DR   GO; GO:0009615; P:response to virus; TAS.
DR   GO; GO:0007165; P:signal transduction; TAS.
DR   InterPro; IPR002473; C-X-C/Interlkn_8.
DR   InterPro; IPR001811; Chemokine_IL8.
DR   InterPro; IPR001089; CXC_chmkine_smll.
DR   Pfam; PF00048; IL8; 1.
DR   PRINTS; PR00436; INTERLEUKIN8.
DR   PROSITE; PS00471; SMALL_CYTOKINES_CXC; FALSE_NEG.
KW   3D-structure; Alternative splicing; Chemotaxis; Cytokine;
KW   Growth factor; Sensory transduction; Signal.
FT   SIGNAL        1     21       Potential.
FT   CHAIN        22     93       Stromal cell-derived factor 1.
FT   CHAIN        24     93       SDF-1-beta(3-72).
FT   CHAIN        24     88       SDF-1-alpha(3-67).
FT   DISULFID     30     55
FT   DISULFID     32     71
FT   VARSPLIC     90     93       Missing (in isoform Alpha).
FT                                /FTId=VSP_001056.
FT   STRAND       36     36
FT   HELIX        41     43
FT   STRAND       44     50
FT   TURN         53     54
FT   STRAND       59     63
FT   TURN         64     66

  Query Match             100.0%;  Score 463;  DB 1;  Length 93;
  Best Local Similarity   100.0%;  Pred. No. 6.5e-44;
  Matches   89;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

Qy         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
              |||||||||||||||||||||||||||||
Db         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89


RESULT 4
Q5IT36_HUMAN
ID   Q5IT36_HUMAN PRELIMINARY;      PRT;   119 AA.
AC   Q5IT36;
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DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Stromal cell-derived factor 1 gamma.
GN   Name=CXCL12;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Callebaut C., Verdin E.;
RT   "Inhibition of X4 and R5 HIV-1 by human SDF-1g, a novel chemokine that
RT   interferes with HIV transcription.";
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY644456; AAT76437.1; -; mRNA.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0008009; F:chemokine activity; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR002473; C-X-C/Interlkn_8.
DR   InterPro; IPR001811; Chemokine_IL8.
DR   Pfam; PF00048; IL8; 1.
DR   PRINTS; PR00436; INTERLEUKIN8.
DR   SMART; SM00199; SCY; 1.
SQ   SEQUENCE   119 AA;  13705 MW;  C36297D68341B824 CRC64;

  Query Match             100.0%;  Score 463;  DB 2;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 8.3e-44;
  Matches   89;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

Qy         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
              |||||||||||||||||||||||||||||
Db         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89


RESULT 5
Q8HYP0_MACMU
ID   Q8HYP0_MACMU PRELIMINARY;      PRT;    89 AA.
AC   Q8HYP0;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Chemokine CXCL12/SDF-1ALPHA.
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC   Cercopithecidae; Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22123042; PubMed=12126650; DOI=10.1006/cyto.2002.0875;
RA   Basu S., Schaefer T.M., Ghosh M., Fuller C.L., Reinhart T.A.;
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RT   "Molecular cloning and sequencing of 25 different rhesus macaque
RT   chemokine cDNAs reveals evolutionary conservation among C, CC, CXC,
RT   and CX3C families of chemokines.";
RL   Cytokine 18:140-148(2002).
DR   EMBL; AF449283; AAN76086.1; -; mRNA.
DR   HSSP; P48061; 1SDF.
DR   SMR; Q8HYP0; 23-88.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0008009; F:chemokine activity; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR002473; C-X-C/Interlkn_8.
DR   InterPro; IPR001811; Chemokine_IL8.
DR   Pfam; PF00048; IL8; 1.
DR   PRINTS; PR00436; INTERLEUKIN8.
DR   SMART; SM00199; SCY; 1.
SQ   SEQUENCE   89 AA;  10105 MW;  AD531633C6DC2B07 CRC64;

  Query Match             98.3%;  Score 455;  DB 2;  Length 89;
  Best Local Similarity   97.8%;  Pred. No. 4.9e-43;
  Matches   87;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
              ||||||||| |||| ||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNAKVVVVLALVLTTLCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

Qy         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
              |||||||||||||||||||||||||||||
Db         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89


RESULT 6
Q5R8M6_PONPY
ID   Q5R8M6_PONPY PRELIMINARY;      PRT;    93 AA.
AC   Q5R8M6;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Hypothetical protein DKFZp469G1525.
GN   Name=DKFZp469G1525;
OS   Pongo pygmaeus (Orangutan).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Pongo.
OX   NCBI_TaxID=9600;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Kidney;
RG   The German cDNA Consortium;
RA   Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA   Fobo G., Han M., Wiemann S.;
RL   Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; CR859725; CAH91884.1; -; mRNA.
DR   SMR; Q5R8M6; 23-88.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0008009; F:chemokine activity; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR002473; C-X-C/Interlkn_8.
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DR   InterPro; IPR001811; Chemokine_IL8.
DR   Pfam; PF00048; IL8; 1.
DR   PRINTS; PR00436; INTERLEUKIN8.
DR   SMART; SM00199; SCY; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   93 AA;  10655 MW;  551D6828FFF9183D CRC64;

  Query Match             96.5%;  Score 447;  DB 2;  Length 93;
  Best Local Similarity   96.6%;  Pred. No. 4.1e-42;
  Matches   86;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
              |||||| || ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNAKVVDVLALVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

Qy         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
              |||||:|||||||||||||||||||||||
Db         61 ARLKNDNRQVCIDPKLKWIQEYLEKALNK 89


RESULT 7
Q54AJ3_FELCA
ID   Q54AJ3_FELCA PRELIMINARY;      PRT;    89 AA.
AC   Q54AJ3;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Stromal cell-derived factor-1 a precursor.
GN   Name=SDF-1a;
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
OC   Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Thymus;
RA   Nishimura Y., Miyazawa T., Ikeda Y., Izumiya Y., Nakamura K., Cai J.,
RA   Sato E., Kohmoto M., Mikami T.;
RT   "Molecular cloning and sequencing of feline stromal cell-derived
RT   factor-1 a and b.";
RL   Eur. J. Immunogenet. 0:0-0(1998).
DR   EMBL; AB011965; BAA28601.1; -; mRNA.
KW   Signal.
FT   SIGNAL        1     18       Potential.
FT   CHAIN        19     89       stromal cell-derived factor-1a.
SQ   SEQUENCE   89 AA;  10018 MW;  81E9BE373B2F85FD CRC64;

  Query Match             96.1%;  Score 445;  DB 2;  Length 89;
  Best Local Similarity   95.5%;  Pred. No. 6.5e-42;
  Matches   85;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
              |:|||| || ||| ||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDAKVVAVLALVLAALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

Qy         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
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                    ||||||||||||||||||||||||||||
Db          61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89


RESULT 8
SDF1_FELCA
ID   SDF1_FELCA     STANDARD;      PRT;    93 AA.
AC   O62657;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Stromal cell-derived factor 1 precursor (SDF-1) (CXCL12).
GN   Name=CXCL12; Synonyms=SDF1;
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
OC   Felinae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   NUCLEOTIDE SEQUENCE (ISOFORMS ALPHA AND BETA).
RC   TISSUE=Thymus;
RX   MEDLINE=98450506; PubMed=9777331;
RX   DOI=10.1046/j.1365-2370.1998.00107.x;
RA   Nishimura Y., Miyazawa T., Ikeda Y., Izumiya Y., Nakamura K.,
RA   Cai J.S., Sato E., Kohmoto M., Mikami T.;
RT   "Molecular cloning and sequencing of feline stromal cell-derived
RT   factor-1 alpha and beta.";
RL   Eur. J. Immunogenet. 25:303-305(1998).
CC   -!- FUNCTION: Chemoattractant active on T-lymphocytes, monocytes, but
CC       not neutrophils.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=Beta;
CC         IsoId=O62657-1; Sequence=Displayed;
CC       Name=Alpha;
CC         IsoId=O62657-2; Sequence=VSP_001055;
CC   -!- SIMILARITY: Belongs to the intercrine alpha (chemokine CxC)
CC       family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; AB011966; BAA28602.1; -; mRNA.
DR   HSSP; P48061; 1SDF.
DR   SMR; O62657; 23-88.
DR   InterPro; IPR002473; C-X-C/Interlkn_8.
DR   InterPro; IPR001811; Chemokine_IL8.
DR   InterPro; IPR001089; CXC_chmkine_sml1.
DR   Pfam; PF00048; IL8; 1.
DR   PRINTS; PR00436; INTERLEUKIN8.
DR   SMART; SM00199; SCY; 1.
DR   PROSITE; PS00471; SMALL_CYTOKINES_CXC; FALSE_NEG.
KW   Alternative splicing; Chemotaxis; Cytokine; Growth factor;
```

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KW   Sensory transduction; Signal.
FT   SIGNAL        1     21       Potential.
FT   CHAIN        22     93       Stromal cell-derived factor 1.
FT   DISULFID     30     55       By similarity.
FT   DISULFID     32     71       By similarity.
FT   VARSPLIC     90     93       Missing (in isoform Alpha).
FT                                /FTId=VSP_001055.
SQ   SEQUENCE   93 AA;  10581 MW;  44FC763711E9BE37 CRC64;

  Query Match             96.1%;  Score 445;  DB 1;  Length 93;
  Best Local Similarity   95.5%;  Pred. No. 6.8e-42;
  Matches   85;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
              |:|||| || ||| ||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MDAKVVAVLALVLAALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

Qy         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
              |||||||||||||||||||||||||||||
Db         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89


RESULT 9
SDF1_MOUSE
ID   SDF1_MOUSE     STANDARD;      PRT;    89 AA.
AC   P40224;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Stromal cell-derived factor 1 precursor (SDF-1) (CXCL12) (Pre-B cell
DE   growth stimulating factor) (PBSF) (12-O-tetradecanoylphorbol 13-
DE   acetate repressed protein 1) (TPAR1) (Thymic lymphoma cell stimulating
DE   factor) (TLSF).
GN   Name=Cxcl12; Synonyms=Sdf1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=94181581; PubMed=8134392;
RA   Nagasawa T., Kikutani H., Kishimoto T.;
RT   "Molecular cloning and structure of a pre-B-cell growth-stimulating
RT   factor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 91:2305-2309(1994).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=93342488; PubMed=8342023;
RA   Tashiro K., Tada H., Heilker R., Shirozu M., Nakano T., Honjo T.;
RT   "Signal sequence trap: a cloning strategy for secreted proteins and
RT   type I membrane proteins.";
RL   Science 261:600-603(1993).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=95073497; PubMed=7982471; DOI=10.1006/excr.1994.1344;
RA   Jiang W., Zhou P., Kahn S.M., Tomita N., Johnson M.D., Weinstein I.B.;
```

RT "Molecular cloning of TPAR1, a gene whose expression is repressed by
RT the tumor promoter 12-O-tetradecanoylphorbol 13-acetate (TPA).";
RL Exp. Cell Res. 215:284-293(1994).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AKR/J;
RA Nomura M., Nakata Y., Uzawa A., Nose M., Akashi M., Suzuki G.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM ALPHA).
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [6]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM ALPHA).
RC STRAIN=C57BL/6J; TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Chemoattractant active on T-lymphocytes, monocytes, but
CC not neutrophils.
CC -!- FUNCTION: Stimulates the proliferation of bone marrow-derived b
CC progenitor cells in the presence of IL-7 as well as growth of the
CC stromal cell-dependent B-cell clone DW34 cells.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Alpha;
CC IsoId=P40224-1; Sequence=Displayed;
CC Name=Beta;
CC IsoId=P40224-2; Sequence=VSP_001057;
CC -!- SIMILARITY: Belongs to the intercrine alpha (chemokine CxC)
CC family.

DR EMBL; D21072; BAA04648.1; -; mRNA.
DR EMBL; L12029; AAA40100.1; -; mRNA.
DR EMBL; L12030; AAA40101.1; -; mRNA.
DR EMBL; S74318; AAB32650.1; -; mRNA.
DR EMBL; D43804; BAA07862.1; -; mRNA.
DR EMBL; D43805; BAA07863.1; -; mRNA.
DR EMBL; AK075596; BAC35845.1; -; mRNA.
DR EMBL; BC006640; AAH06640.1; -; mRNA.
DR PIR; A53497; A53497.
DR PIR; I81182; I81182.
DR HSSP; P48061; 1SDF.
DR SMR; P40224; 23-88.
DR Ensembl; ENSMUSG00000061353; Mus musculus.
DR MGI; MGI:103556; Cxcl12.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0008009; F:chemokine activity; IDA.
DR GO; GO:0007420; P:brain development; IDA.
DR GO; GO:0007281; P:germ cell development; IDA.
DR GO; GO:0008354; P:germ cell migration; IDA.
DR GO; GO:0050930; P:induction of positive chemotaxis; IDA.
DR GO; GO:0030335; P:positive regulation of cell migration; IDA.
DR GO; GO:0042098; P:T cell proliferation; IMP.
DR InterPro; IPR002473; C-X-C/Interlkn_8.
DR InterPro; IPR001811; Chemokine_IL8.
DR InterPro; IPR001089; CXC_chmkine_smll.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00436; INTERLEUKIN8.
DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; FALSE_NEG.

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KW   Alternative splicing; Chemotaxis; Cytokine; Growth factor;
KW   Sensory transduction; Signal.
FT   SIGNAL        1     21       Potential.
FT   CHAIN        22     89       Stromal cell-derived factor 1.
FT   DISULFID     30     55       By similarity.
FT   DISULFID     32     71       By similarity.
FT   VARSPLIC     89     89       K -> KRLKM (in isoform Beta).
FT                                /FTId=VSP_001057.
SQ   SEQUENCE   89 AA;  10032 MW;  C4B8AD69078E55FA CRC64;

  Query Match             95.5%;  Score 442;  DB 1;  Length 89;
  Best Local Similarity   93.3%;  Pred. No. 1.4e-41;
  Matches   83;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
              |:|||| || ||| |||:||||||||||||||||||:||||||||||||||||||||||
Db          1 MDAKVVAVLALVLAALCISDGKPVSLSYRCPCRFFESHIARANVKHLKILNTPNCALQIV 60

Qy         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
              |||||||||||||||||||||||||||||
Db         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89


RESULT 10
Q543V6_MOUSE
ID   Q543V6_MOUSE PRELIMINARY;      PRT;    89 AA.
AC   Q543V6;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   9.5 days embryo parthenogenote cDNA, RIKEN full-length enriched
DE   library, clone:B130032A21 product:stromal cell derived factor 1, full
DE   insert sequence.
GN   Name=Cxcl12;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Parthenogenote;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Parthenogenote;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
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RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Parthenogenote;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.

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RC   STRAIN=C57BL/6J; TISSUE=Parthenogenote;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Parthenogenote;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK045092; BAC32216.1; -; mRNA.
DR   MGI; MGI:103556; Cxcl12.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0008009; F:chemokine activity; IDA.
DR   GO; GO:0007420; P:brain development; IDA.
DR   GO; GO:0007281; P:germ cell development; IDA.
DR   GO; GO:0008354; P:germ cell migration; IDA.
DR   GO; GO:0050930; P:induction of positive chemotaxis; IDA.
DR   GO; GO:0030335; P:positive regulation of cell migration; IDA.
DR   GO; GO:0042098; P:T cell proliferation; IMP.
SQ   SEQUENCE   89 AA;  10032 MW;  C4B8AD69078E55FA CRC64;

  Query Match             95.5%;  Score 442;  DB 2;  Length 89;
  Best Local Similarity   93.3%;  Pred. No. 1.4e-41;
  Matches   83;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
              |:|||| || ||| |||:||||||||||||||||:||||||||||||||||||||
Db          1 MDAKVVAVLALVLAALCISDGKPVSLSYRCPCRFFESHIARANVKHLKILNTPNCALQIV 60

Qy         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
              ||||||||||||||||||||||||||||
Db         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89


RESULT 11
Q4FJL5_MOUSE
ID   Q4FJL5_MOUSE PRELIMINARY;      PRT;    93 AA.
AC   Q4FJL5;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
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DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Cxcl12 protein.
GN   Name=Cxcl12;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Ebert L., Muenstermann E., Schatten R., Henze S., Bohn E.,
RA   Mollenhauer J., Wiemann S., Schick M., Korn B.;
RT   "Cloning of mouse full open reading frames in Gateway(R) system entry
RT   vector (pDONR201).";
RL   Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; CT010389; CAJ18596.1; -; mRNA.
SQ   SEQUENCE   93 AA;  10561 MW;  625367D344B8AD69 CRC64;

  Query Match             95.5%;  Score 442;  DB 2;  Length 93;
  Best Local Similarity   93.3%;  Pred. No. 1.5e-41;
  Matches   83;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
              |:|||| || ||| |||:||||||||||||||||||:||||||||||||||||||||
Db          1 MDAKVVAVLALVLAALCISDGKPVSLSYRCPCRFFESHIARANVKHLKILNTPNCALQIV 60

Qy         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
              |||||||||||||||||||||||||||||
Db         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89


RESULT 12
Q80ZW4_MOUSE
ID   Q80ZW4_MOUSE PRELIMINARY;      PRT;   137 AA.
AC   Q80ZW4;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Cxcl12 protein.
GN   Name=Cxcl12;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6; TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
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RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6; TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC046827; AAH46827.1; -; mRNA.
DR   HSSP; P48061; 1SDF.
DR   SMR; Q80ZW4; 23-88.
DR   MGI; MGI:103556; Cxcl12.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0008009; F:chemokine activity; IDA.
DR   GO; GO:0007420; P:brain development; IDA.
DR   GO; GO:0007281; P:germ cell development; IDA.
DR   GO; GO:0008354; P:germ cell migration; IDA.
DR   GO; GO:0050930; P:induction of positive chemotaxis; IDA.
DR   GO; GO:0030335; P:positive regulation of cell migration; IDA.
DR   GO; GO:0042098; P:T-cell proliferation; IMP.
DR   InterPro; IPR002473; C-X-C/Interlkn_8.
DR   InterPro; IPR001811; Chemokine_IL8.
DR   Pfam; PF00048; IL8; 1.
DR   PRINTS; PR00436; INTERLEUKIN8.
DR   SMART; SM00199; SCY; 1.
SQ   SEQUENCE   137 AA;  15529 MW;  04B47DAB6904DF77 CRC64;

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  Best Local Similarity   93.3%;  Pred. No. 2.1e-41;
  Matches   83;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

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Qy         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
              |||||||||||||||||||||||||||||
Db         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89


RESULT 13
Q5XNN9_CANFA
ID   Q5XNN9_CANFA PRELIMINARY;      PRT;    89 AA.
AC   Q5XNN9;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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DE   Stromal cell-derived factor-1.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC   Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Wei Y., Hu S.;
RT   "Identification and cloning of dog SDF-1 cDNA.";
RL   Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY746395; AAU89475.2; -; mRNA.
DR   SMR; Q5XNN9; 23-88.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0008009; F:chemokine activity; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR002473; C-X-C/Interlkn_8.
DR   InterPro; IPR001811; Chemokine_IL8.
DR   Pfam; PF00048; IL8; 1.
DR   PRINTS; PR00436; INTERLEUKIN8.
DR   SMART; SM00199; SCY; 1.
SQ   SEQUENCE   89 AA;  10005 MW;  E9B8AD69078E4020 CRC64;

  Query Match             94.4%;  Score 437;  DB 2;  Length 89;
  Best Local Similarity   92.1%;  Pred. No. 5.1e-41;
  Matches   82;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
              |:|||| || ||| |||:||||||||||||||||||:||||||||||||||||||||||
Db          1 MDAKVVAVLALVLAALCISDGKPVSLSYRCPCRFFESHIARANVKHLKILNTPNCALQIV 60

Qy         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
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Db         61 ARLKNNSRQVCIDPKLKWIQEYLEKALNK 89


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AC   Q9QZD1;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Stromal cell-derived factor-1 alpha (Chemokine (C-X-C motif) ligand
DE   12).
GN   Name=Cxcl12; Synonyms=SDF-1;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Sprague-Dawley;
RA   Ohtani Y., Okada M., Kawaguchi N., Minami M., Satoh M.;
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
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RP NUCLEOTIDE SEQUENCE.
RA Pillarisetti K., Gupta S.K.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RA Director MGC Project;
RL Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF189724; AAF01066.1; -; mRNA.
DR EMBL; AF209976; AAG43506.1; -; mRNA.
DR EMBL; BC078737; AAH78737.1; -; mRNA.
DR HSSP; P48061; 1SDF.
DR SMR; Q9QZD1; 23-88.
DR Ensembl; ENSRNOG00000013589; Rattus norvegicus.
DR RGD; 3651; Cxcl12.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR002473; C-X-C/Interlkn_8.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR00436; INTERLEUKIN8.
DR SMART; SM00199; SCY; 1.
SQ SEQUENCE 89 AA; 9977 MW; D86977626A2E35FA CRC64;

Query Match 94.0%; Score 435; DB 2; Length 89;
Best Local Similarity 92.1%; Pred. No. 8.6e-41;
Matches 82; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

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Db          61 ARLKSNNRQVCIDPKLKWIQEYLDKALNK 89


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ID   Q80YV8_RAT  PRELIMINARY;      PRT;   119 AA.
AC   Q80YV8;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Stromal cell-derived factor-1 gamma.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Gleichmann M., Gillen C., Mueller H.W.;
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF217564; AAF63712.1; -; mRNA.
DR   HSSP; P48061; 1SDF.
DR   SMR; Q80YV8; 23-88.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0008009; F:chemokine activity; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR002473; C-X-C/Interlkn_8.
DR   InterPro; IPR001811; Chemokine_IL8.
DR   Pfam; PF00048; IL8; 1.
DR   PRINTS; PR00436; INTERLEUKIN8.
DR   SMART; SM00199; SCY; 1.
SQ   SEQUENCE   119 AA;  13551 MW;  5E1D99E44DC36FA8 CRC64;

  Query Match             94.0%;  Score 435;  DB 2;  Length 119;
  Best Local Similarity   92.1%;  Pred. No. 1.1e-40;
  Matches   82;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

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               |:|||| || ||| |||:||||||||||||||||||||||||||||||||||||||||
Db           1 MDAKVVAVLALVLAALCISDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

Qy          61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
               ||||:||||||||||||||||:|||||
Db          61 ARLKSNNRQVCIDPKLKWIQEYLDKALNK 89


Search completed: April 26, 2006, 02:37:30
Job time : 228 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 26, 2006, 02:39:19 ; Search time 25 Seconds
(without alignments)
156.650 Million cell updates/sec

Title: US-10-785-230-5
Perfect score: 463
Sequence: 1 MNAKVVVVLVLVLTALCLSD.....VCIDPKLKWIQEYLEKALNK 89

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 225428 seqs, 44002918 residues

Total number of hits satisfying chosen parameters: 225428

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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8: /SIDS5/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	463	100.0	89	6	US-10-241-375-22	Sequence 22, Appl
2	463	100.0	89	7	US-11-028-922A-6	Sequence 6, Appli
3	463	100.0	93	6	US-10-241-375-56	Sequence 56, Appl
4	435	94.0	89	7	US-11-028-922A-7	Sequence 7, Appli
5	365	78.8	72	7	US-11-136-097-7	Sequence 7, Appli
6	360	77.8	67	7	US-11-136-097-6	Sequence 6, Appli
7	359	77.5	68	7	US-11-028-922A-5	Sequence 5, Appli
8	351	75.8	67	6	US-10-945-674A-1	Sequence 1, Appli
9	347	74.9	67	6	US-10-945-674A-7	Sequence 7, Appli

10	346	74.7	67	6	US-10-945-674A-3	Sequence 3, Appli
11	346	74.7	67	6	US-10-945-674A-6	Sequence 6, Appli
12	345	74.5	67	6	US-10-945-674A-9	Sequence 9, Appli
13	344	74.3	67	6	US-10-945-674A-2	Sequence 2, Appli
14	344	74.3	67	6	US-10-945-674A-5	Sequence 5, Appli
15	343	74.1	67	6	US-10-945-674A-8	Sequence 8, Appli
16	343	74.1	67	6	US-10-945-674A-133	Sequence 133, App
17	342	73.9	67	6	US-10-945-674A-10	Sequence 10, Appl
18	341	73.7	67	6	US-10-945-674A-4	Sequence 4, Appli
19	339	73.2	67	6	US-10-945-674A-11	Sequence 11, Appl
20	337	72.8	67	6	US-10-945-674A-12	Sequence 12, Appl
21	127.5	27.5	34	6	US-10-945-674A-75	Sequence 75, Appl
22	127.5	27.5	34	6	US-10-945-674A-124	Sequence 124, App
23	127.5	27.5	34	6	US-10-945-674A-126	Sequence 126, App
24	123.5	26.7	34	6	US-10-945-674A-100	Sequence 100, App
25	122.5	26.5	34	6	US-10-945-674A-84	Sequence 84, Appl
26	122.5	26.5	34	6	US-10-945-674A-99	Sequence 99, Appl
27	121.5	26.2	34	6	US-10-945-674A-102	Sequence 102, App
28	120.5	26.0	34	6	US-10-945-674A-83	Sequence 83, Appl
29	120.5	26.0	34	6	US-10-945-674A-86	Sequence 86, Appl
30	119.5	25.8	34	6	US-10-945-674A-101	Sequence 101, App
31	118.5	25.6	34	6	US-10-945-674A-114	Sequence 114, App
32	117.5	25.4	34	6	US-10-945-674A-85	Sequence 85, Appl
33	115.5	24.9	34	6	US-10-945-674A-115	Sequence 115, App
34	113.5	24.5	34	6	US-10-945-674A-116	Sequence 116, App
35	113	24.4	99	6	US-10-241-375-23	Sequence 23, Appl
36	113	24.4	99	7	US-11-186-284-87	Sequence 87, Appl
37	108	23.3	31	6	US-10-945-674A-74	Sequence 74, Appl
38	108	23.3	31	6	US-10-945-674A-123	Sequence 123, App
39	108	23.3	31	6	US-10-945-674A-125	Sequence 125, App
40	106.5	23.0	91	6	US-10-241-375-21	Sequence 21, Appl
41	106.5	23.0	91	7	US-11-262-284-21	Sequence 21, Appl
42	104	22.5	31	6	US-10-945-674A-96	Sequence 96, Appl
43	103	22.2	31	6	US-10-945-674A-80	Sequence 80, Appl
44	103	22.2	31	6	US-10-945-674A-95	Sequence 95, Appl
45	102	22.0	31	6	US-10-945-674A-98	Sequence 98, Appl

ALIGNMENTS

RESULT 1
US-10-241-375-22
; Sequence 22, Application US/10241375
; Publication No. US20060073114A1
; GENERAL INFORMATION:
; APPLICANT: Grainger, David J.
; APPLICANT: Tatalick, Lauen Marie
; APPLICANT: Kanaly, Suzanne T.
; TITLE OF INVENTION: Compounds and methods to inhibit or
; TITLE OF INVENTION: augment an inflammatory response.
; FILE REFERENCE: 295.027US1
; CURRENT APPLICATION NUMBER: US/10/241,375
; CURRENT FILING DATE: 2002-09-11
; PRIOR APPLICATION NUMBER: US/09/150,813
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: US 08/927939

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;  PRIOR FILING DATE: 1997-09-11
;  NUMBER OF SEQ ID NOS: 105
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 22
;   LENGTH: 89
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-241-375-22

  Query Match             100.0%;  Score 463;  DB 6;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 4.9e-49;
  Matches   89;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
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Db          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

Qy         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
              |||||||||||||||||||||||||||||
Db         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89


RESULT 2
US-11-028-922A-6
; Sequence 6, Application US/11028922A
; Publication No. US20050271639A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Marc
;  TITLE OF INVENTION: GENETICALLY ENGINEERED FOR THERAPEUTIC APPLICATIONS
;  FILE REFERENCE: CCF-7019
;  CURRENT APPLICATION NUMBER: US/11/028,922A
;  CURRENT FILING DATE:  2005-01-04
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
;   LENGTH: 89
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-028-922A-6

  Query Match             100.0%;  Score 463;  DB 7;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 4.9e-49;
  Matches   89;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

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Db         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89


RESULT 3
US-10-241-375-56
; Sequence 56, Application US/10241375
; Publication No. US20060073114A1
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; GENERAL INFORMATION:
; APPLICANT: Grainger, David J.
; APPLICANT: Tatalick, Lauen Marie
; APPLICANT: Kanaly, Suzanne T.
; TITLE OF INVENTION: Compounds and methods to inhibit or
; TITLE OF INVENTION: augment an inflammatory response.
; FILE REFERENCE: 295.027US1
; CURRENT APPLICATION NUMBER: US/10/241,375
; CURRENT FILING DATE: 2002-09-11
; PRIOR APPLICATION NUMBER: US/09/150,813
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: US 08/927939
; PRIOR FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 56
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-241-375-56

Query Match 100.0%; Score 463; DB 6; Length 93;
Best Local Similarity 100.0%; Pred. No. 5.2e-49;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
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Qy 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
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Db 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89

RESULT 4
US-11-028-922A-7
; Sequence 7, Application US/11028922A
; Publication No. US20050271639A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Marc
; TITLE OF INVENTION: GENETICALLY ENGINEERED FOR THERAPEUTIC APPLICATIONS
; FILE REFERENCE: CCF-7019
; CURRENT APPLICATION NUMBER: US/11/028,922A
; CURRENT FILING DATE: 2005-01-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-11-028-922A-7

Query Match 94.0%; Score 435; DB 7; Length 89;
Best Local Similarity 92.1%; Pred. No. 1.2e-45;
Matches 82; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

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              |:|||| || ||| |||:|||||||||||||||||||||||||||||||||||||||||
Db          1 MDAKVVAVLALVLAALCISDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

Qy         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
              ||||:||||||||||||||||:|||||
Db         61 ARLKSNNRQVCIDPKLKWIQEYLDKALNK 89


RESULT 5
US-11-136-097-7
; Sequence 7, Application US/11136097
; Publication No. US20050265969A1
; GENERAL INFORMATION:
;  APPLICANT: Clark-Lewis, Ian
;  APPLICANT:  Gong, Jiang-Hong
;  APPLICANT:  Duronio, Vincent
;  APPLICANT:  The University of British Columbia
;  TITLE OF INVENTION: Therapeutic Chemokine Receptor Antagonists
;  FILE REFERENCE: 080352-000000US
;  CURRENT APPLICATION NUMBER: US/11/136,097
;  CURRENT FILING DATE:  2005-05-23
;  PRIOR APPLICATION NUMBER: US/09/646,192
;  PRIOR FILING DATE: 2000-09-13
;  PRIOR APPLICATION NUMBER: CA 2,226,391
;  PRIOR FILING DATE: 1998-03-13
;  PRIOR APPLICATION NUMBER: CA 2,245,224
;  PRIOR FILING DATE: 1998-08-14
;  PRIOR APPLICATION NUMBER: WO PCT/CA99/00221
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 72
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: stromal cell derived factor-1beta (SDF-1beta)
US-11-136-097-7

  Query Match             78.8%;  Score 365;  DB 7;  Length 72;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-37;
  Matches   68;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         22 KPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIQE 81
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 KPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIQE 60

Qy         82 YLEKALNK 89
              ||||||||
Db         61 YLEKALNK 68


RESULT 6
US-11-136-097-6
; Sequence 6, Application US/11136097
; Publication No. US20050265969A1
; GENERAL INFORMATION:
```

```
;  APPLICANT: Clark-Lewis, Ian
;  APPLICANT:  Gong, Jiang-Hong
;  APPLICANT:  Duronio, Vincent
;  APPLICANT:  The University of British Columbia
;  TITLE OF INVENTION: Therapeutic Chemokine Receptor Antagonists
;  FILE REFERENCE: 080352-000000US
;  CURRENT APPLICATION NUMBER: US/11/136,097
;  CURRENT FILING DATE:  2005-05-23
;  PRIOR APPLICATION NUMBER: US/09/646,192
;  PRIOR FILING DATE: 2000-09-13
;  PRIOR APPLICATION NUMBER: CA 2,226,391
;  PRIOR FILING DATE: 1998-03-13
;  PRIOR APPLICATION NUMBER: CA 2,245,224
;  PRIOR FILING DATE: 1998-08-14
;  PRIOR APPLICATION NUMBER: WO PCT/CA99/00221
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 67
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: stromal cell derived factor-1alpha (SDF-1alpha)
US-11-136-097-6

  Query Match             77.8%;  Score 360;  DB 7;  Length 67;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-36;
  Matches   67;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         22 KPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIQE 81
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 KPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIQE 60

Qy         82 YLEKALN 88
              |||||||
Db         61 YLEKALN 67


RESULT 7
US-11-028-922A-5
; Sequence 5, Application US/11028922A
; Publication No. US20050271639A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Marc
;  TITLE OF INVENTION: GENETICALLY ENGINEERED FOR THERAPEUTIC APPLICATIONS
;  FILE REFERENCE: CCF-7019
;  CURRENT APPLICATION NUMBER: US/11/028,922A
;  CURRENT FILING DATE:  2005-01-04
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
;   LENGTH: 68
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-028-922A-5
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  Query Match             77.5%;  Score 359;  DB 7;  Length 68;
  Best Local Similarity   98.5%;  Pred. No. 1.5e-36;
  Matches   67;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         22 KPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIQE 81
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 KPVSLLYRCPCRFFESHVARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIQE 60

Qy         82 YLEKALNK 89
              ||||||||
Db         61 YLEKALNK 68


RESULT 8
US-10-945-674A-1
; Sequence 1, Application US/10945674A
; Publication No. US20060014682A1
; GENERAL INFORMATION:
;  APPLICANT: Tudan, Christopher R.
;  APPLICANT:  Merzouk, Ahmed
;  APPLICANT:  Arab, Lakhdar
;  APPLICANT:  Saxena, Geeta
;  APPLICANT:  Eaves, Connie J.
;  APPLICANT:  Cashman, Joanne
;  APPLICANT:  Clark-Lewis, Ian
;  APPLICANT:  Salari, Hassan
;  APPLICANT:  Chemokine Therapeutics Corporation
;  APPLICANT:  The University of British Columbia
;  TITLE OF INVENTION: CXCR4 Antagonist Treatment of Hematopoietic Cells
;  FILE REFERENCE: 080420-000100US
;  CURRENT APPLICATION NUMBER: US/10/945,674A
;  CURRENT FILING DATE:  2004-09-20
;  PRIOR APPLICATION NUMBER: CA 2,305,787
;  PRIOR FILING DATE: 2000-05-09
;  PRIOR APPLICATION NUMBER: US 60/205,467
;  PRIOR FILING DATE: 2000-05-19
;  PRIOR APPLICATION NUMBER: US 09/852,424
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 140
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 67
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:synthetic
;   OTHER INFORMATION: SDF-1(1-67)[P2G] CXCR4 receptor antagonist
US-10-945-674A-1

  Query Match             75.8%;  Score 351;  DB 6;  Length 67;
  Best Local Similarity   98.5%;  Pred. No. 1.3e-35;
  Matches   66;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         22 KPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIQE 81
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 KGVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIQE 60
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```
Qy          82 YLEKALN 88
               |||||||
Db          61 YLEKALN 67


RESULT 9
US-10-945-674A-7
; Sequence 7, Application US/10945674A
; Publication No. US20060014682A1
; GENERAL INFORMATION:
;  APPLICANT: Tudan, Christopher R.
;  APPLICANT:  Merzouk, Ahmed
;  APPLICANT:  Arab, Lakhdar
;  APPLICANT:  Saxena, Geeta
;  APPLICANT:  Eaves, Connie J.
;  APPLICANT:  Cashman, Joanne
;  APPLICANT:  Clark-Lewis, Ian
;  APPLICANT:  Salari, Hassan
;  APPLICANT:  Chemokine Therapeutics Corporation
;  APPLICANT:  The University of British Columbia
;  TITLE OF INVENTION: CXCR4 Antagonist Treatment of Hematopoietic Cells
;  FILE REFERENCE: 080420-000100US
;  CURRENT APPLICATION NUMBER: US/10/945,674A
;  CURRENT FILING DATE:  2004-09-20
;  PRIOR APPLICATION NUMBER: CA 2,305,787
;  PRIOR FILING DATE: 2000-05-09
;  PRIOR APPLICATION NUMBER: US 60/205,467
;  PRIOR FILING DATE: 2000-05-19
;  PRIOR APPLICATION NUMBER: US 09/852,424
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 140
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 67
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:synthetic
;   OTHER INFORMATION: SDF-1[P2G] CXCR4 receptor antagonist analogue
;   OTHER INFORMATION: with proline-amino acid chimera (P*) substituted
;   OTHER INFORMATION: at residue 6
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (6)
;   OTHER INFORMATION: Xaa = P* = proline-amino acid chimera (3-aryl-proline,
;   OTHER INFORMATION: 3-hydroxyaryl-proline or 3-alkyl-proline)
US-10-945-674A-7

  Query Match             74.9%;  Score 347;  DB 6;  Length 67;
  Best Local Similarity   97.0%;  Pred. No. 4.1e-35;
  Matches   65;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          22 KPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIQE 81
               | ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 KGVSLXYRCPCRFFESHVARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIQE 60

Qy          82 YLEKALN 88
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                  |||||||
Db          61 YLEKALN 67


RESULT 10
US-10-945-674A-3
; Sequence 3, Application US/10945674A
; Publication No. US20060014682A1
; GENERAL INFORMATION:
;  APPLICANT: Tudan, Christopher R.
;  APPLICANT:  Merzouk, Ahmed
;  APPLICANT:  Arab, Lakhdar
;  APPLICANT:  Saxena, Geeta
;  APPLICANT:  Eaves, Connie J.
;  APPLICANT:  Cashman, Joanne
;  APPLICANT:  Clark-Lewis, Ian
;  APPLICANT:  Salari, Hassan
;  APPLICANT:  Chemokine Therapeutics Corporation
;  APPLICANT:  The University of British Columbia
;  TITLE OF INVENTION: CXCR4 Antagonist Treatment of Hematopoietic Cells
;  FILE REFERENCE: 080420-000100US
;  CURRENT APPLICATION NUMBER: US/10/945,674A
;  CURRENT FILING DATE:  2004-09-20
;  PRIOR APPLICATION NUMBER: CA 2,305,787
;  PRIOR FILING DATE: 2000-05-09
;  PRIOR APPLICATION NUMBER: US 60/205,467
;  PRIOR FILING DATE: 2000-05-19
;  PRIOR APPLICATION NUMBER: US 09/852,424
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 140
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 67
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:synthetic
;   OTHER INFORMATION: SDF-1(1-67)[P2G] CXCR4 receptor antagonist
;   OTHER INFORMATION: analogue with proline (P) substituted at residue 6
US-10-945-674A-3

  Query Match             74.7%;  Score 346;  DB 6;  Length 67;
  Best Local Similarity   97.0%;  Pred. No. 5.4e-35;
  Matches   65;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         22 KPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIQE 81
              | ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 KGVSLPYRCPCRFFESHVARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIQE 60

Qy         82 YLEKALN 88
              |||||||
Db         61 YLEKALN 67


RESULT 11
US-10-945-674A-6
; Sequence 6, Application US/10945674A
```

; Publication No. US20060014682A1
; GENERAL INFORMATION:
; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Arab, Lakhdar
; APPLICANT: Saxena, Geeta
; APPLICANT: Eaves, Connie J.
; APPLICANT: Cashman, Joanne
; APPLICANT: Clark-Lewis, Ian
; APPLICANT: Salari, Hassan
; APPLICANT: Chemokine Therapeutics Corporation
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: CXCR4 Antagonist Treatment of Hematopoietic Cells
; FILE REFERENCE: 080420-000100US
; CURRENT APPLICATION NUMBER: US/10/945,674A
; CURRENT FILING DATE: 2004-09-20
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/852,424
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic
; OTHER INFORMATION: SDF-1[P2G] CXCR4 receptor antagonist analogue
; OTHER INFORMATION: with proline-amino acid chimera (P*) substituted
; OTHER INFORMATION: at residue 5
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)
; OTHER INFORMATION: Xaa = P* = proline-amino acid chimera (3-aryl-proline,
; OTHER INFORMATION: 3-hydroxyaryl-proline or 3-alkyl-proline)
US-10-945-674A-6

Query Match 74.7%; Score 346; DB 6; Length 67;
Best Local Similarity 97.0%; Pred. No. 5.4e-35;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy         22 KPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIQE 81
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 KGVSXSYRCPCRFFESHVARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIQE 60

Qy         82 YLEKALN 88
              |||||||
Db         61 YLEKALN 67
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RESULT 12
US-10-945-674A-9
; Sequence 9, Application US/10945674A
; Publication No. US20060014682A1

; GENERAL INFORMATION:
; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Arab, Lakhdar
; APPLICANT: Saxena, Geeta
; APPLICANT: Eaves, Connie J.
; APPLICANT: Cashman, Joanne
; APPLICANT: Clark-Lewis, Ian
; APPLICANT: Salari, Hassan
; APPLICANT: Chemokine Therapeutics Corporation
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: CXCR4 Antagonist Treatment of Hematopoietic Cells
; FILE REFERENCE: 080420-000100US
; CURRENT APPLICATION NUMBER: US/10/945,674A
; CURRENT FILING DATE: 2004-09-20
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/852,424
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic
; OTHER INFORMATION: SDF-1[P2G] CXCR4 receptor antagonist analogue
; OTHER INFORMATION: with proline-amino acid chimera (P*) substituted
; OTHER INFORMATION: at residue 8
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (8)
; OTHER INFORMATION: Xaa = P* = proline-amino acid chimera (3-aryl-proline,
; OTHER INFORMATION: 3-hydroxyaryl-proline or 3-alkyl-proline)
US-10-945-674A-9

Query Match 74.5%; Score 345; DB 6; Length 67;
Best Local Similarity 97.0%; Pred. No. 7.1e-35;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy         22 KPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIQE 81
              | ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 KGVSLSYXCPCRFFESHVARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIQE 60

Qy         82 YLEKALN 88
              |||||||
Db         61 YLEKALN 67
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RESULT 13
US-10-945-674A-2
; Sequence 2, Application US/10945674A
; Publication No. US20060014682A1
; GENERAL INFORMATION:

; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Arab, Lakhdar
; APPLICANT: Saxena, Geeta
; APPLICANT: Eaves, Connie J.
; APPLICANT: Cashman, Joanne
; APPLICANT: Clark-Lewis, Ian
; APPLICANT: Salari, Hassan
; APPLICANT: Chemokine Therapeutics Corporation
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: CXCR4 Antagonist Treatment of Hematopoietic Cells
; FILE REFERENCE: 080420-000100US
; CURRENT APPLICATION NUMBER: US/10/945,674A
; CURRENT FILING DATE: 2004-09-20
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/852,424
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic
; OTHER INFORMATION: SDF-1(1-67)[P2G] CXCR4 receptor antagonist
; OTHER INFORMATION: analogue with proline (P) substituted at residue 5
US-10-945-674A-2

Query Match 74.3%; Score 344; DB 6; Length 67;
Best Local Similarity 97.0%; Pred. No. 9.4e-35;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy         22 KPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIQE 81
              | || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 KGVSPSYRCPCRFFESHVARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIQE 60

Qy         82 YLEKALN 88
              |||||||
Db         61 YLEKALN 67
```

RESULT 14
US-10-945-674A-5
; Sequence 5, Application US/10945674A
; Publication No. US20060014682A1
; GENERAL INFORMATION:
; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Arab, Lakhdar
; APPLICANT: Saxena, Geeta
; APPLICANT: Eaves, Connie J.
; APPLICANT: Cashman, Joanne
; APPLICANT: Clark-Lewis, Ian

; APPLICANT: Salari, Hassan
; APPLICANT: Chemokine Therapeutics Corporation
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: CXCR4 Antagonist Treatment of Hematopoietic Cells
; FILE REFERENCE: 080420-000100US
; CURRENT APPLICATION NUMBER: US/10/945,674A
; CURRENT FILING DATE: 2004-09-20
; PRIOR APPLICATION NUMBER: CA 2,305,787
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 60/205,467
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/852,424
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic
; OTHER INFORMATION: SDF-1(1-67)[P2G] CXCR4 receptor antagonist
; OTHER INFORMATION: analogue with proline (P) substituted at residue 8
US-10-945-674A-5

Query Match 74.3%; Score 344; DB 6; Length 67;
Best Local Similarity 97.0%; Pred. No. 9.4e-35;
Matches 65; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy         22 KPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIQE 81
              | ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 KGVSLSYPCPCRFFESHVARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIQE 60

Qy         82 YLEKALN 88
              |||||||
Db         61 YLEKALN 67
```

RESULT 15
US-10-945-674A-8
; Sequence 8, Application US/10945674A
; Publication No. US20060014682A1
; GENERAL INFORMATION:
; APPLICANT: Tudan, Christopher R.
; APPLICANT: Merzouk, Ahmed
; APPLICANT: Arab, Lakhdar
; APPLICANT: Saxena, Geeta
; APPLICANT: Eaves, Connie J.
; APPLICANT: Cashman, Joanne
; APPLICANT: Clark-Lewis, Ian
; APPLICANT: Salari, Hassan
; APPLICANT: Chemokine Therapeutics Corporation
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: CXCR4 Antagonist Treatment of Hematopoietic Cells
; FILE REFERENCE: 080420-000100US
; CURRENT APPLICATION NUMBER: US/10/945,674A
; CURRENT FILING DATE: 2004-09-20

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;  PRIOR APPLICATION NUMBER: CA 2,305,787
;  PRIOR FILING DATE: 2000-05-09
;  PRIOR APPLICATION NUMBER: US 60/205,467
;  PRIOR FILING DATE: 2000-05-19
;  PRIOR APPLICATION NUMBER: US 09/852,424
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 140
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 67
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:synthetic
;   OTHER INFORMATION: SDF-1[P2G] CXCR4 receptor antagonist analogue
;   OTHER INFORMATION: with proline-amino acid chimera (P*) substituted
;   OTHER INFORMATION: at residue 7
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (7)
;   OTHER INFORMATION: Xaa = P* = proline-amino acid chimera (3-aryl-proline,
;   OTHER INFORMATION: 3-hydroxyaryl-proline or 3-alkyl-proline)
US-10-945-674A-8

  Query Match             74.1%;  Score 343;  DB 6;  Length 67;
  Best Local Similarity   97.0%;  Pred. No. 1.2e-34;
  Matches   65;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         22 KPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIQE 81
              | |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 KGVSLSXRCPCRFFESHVARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIQE 60

Qy         82 YLEKALN 88
              |||||||
Db         61 YLEKALN 67


Search completed: April 26, 2006, 02:42:27
Job time : 26 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 26, 2006, 02:38:29 ; Search time 165 Seconds
(without alignments)
225.375 Million cell updates/sec

Title: US-10-785-230-5
Perfect score: 463
Sequence: 1 MNAKVVVVLVLVLTALCLSD.....VCIDPKLKWIQEYLEKALNK 89

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

Database : Published_Applications_AA_Main:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	463	100.0	89	2	US-08-927-939-22	Sequence 22, Appl
2	463	100.0	89	3	US-09-953-692-4	Sequence 4, Appli
3	463	100.0	89	3	US-09-953-717-4	Sequence 4, Appli
4	463	100.0	89	3	US-09-792-793A-32	Sequence 32, Appl
5	463	100.0	89	4	US-10-375-209A-32	Sequence 32, Appl
6	463	100.0	89	4	US-10-785-230-5	Sequence 5, Appli
7	463	100.0	89	5	US-10-924-029-1	Sequence 1, Appli
8	463	100.0	89	5	US-10-985-324-4	Sequence 4, Appli
9	463	100.0	89	5	US-10-773-236-280	Sequence 280, App
10	463	100.0	89	5	US-10-921-235-43	Sequence 43, Appl
11	463	100.0	93	2	US-08-927-939-56	Sequence 56, Appl

12	463	100.0	93	3	US-09-144-838-7	Sequence 7, Appli
13	463	100.0	93	3	US-09-919-497-95	Sequence 95, Appl
14	463	100.0	93	3	US-09-835-107-2	Sequence 2, Appli
15	463	100.0	93	3	US-09-835-107-3	Sequence 3, Appli
16	463	100.0	93	3	US-09-792-793A-93	Sequence 93, Appl
17	463	100.0	93	4	US-10-086-177A-2	Sequence 2, Appli
18	463	100.0	93	4	US-10-086-177A-3	Sequence 3, Appli
19	463	100.0	93	4	US-10-375-209A-93	Sequence 93, Appl
20	463	100.0	93	4	US-10-447-315-25	Sequence 25, Appl
21	463	100.0	93	4	US-10-706-265-6	Sequence 6, Appli
22	463	100.0	93	4	US-10-788-792-193	Sequence 193, App
23	463	100.0	93	5	US-10-723-860-2672	Sequence 2672, Ap
24	463	100.0	93	5	US-10-924-029-2	Sequence 2, Appli
25	463	100.0	93	5	US-10-222-703A-3	Sequence 3, Appli
26	463	100.0	93	5	US-10-222-703A-4	Sequence 4, Appli
27	463	100.0	93	5	US-10-849-989-28	Sequence 28, Appl
28	463	100.0	93	5	US-10-756-149-5439	Sequence 5439, Ap
29	463	100.0	93	5	US-10-287-436A-522	Sequence 522, App
30	463	100.0	93	5	US-10-287-436A-1213	Sequence 1213, Ap
31	463	100.0	119	4	US-10-308-322-12	Sequence 12, Appl
32	463	100.0	166	4	US-10-335-394-5	Sequence 5, Appli
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34	435	94.0	93	4	US-10-308-322-17	Sequence 17, Appl
35	435	94.0	119	4	US-10-308-322-13	Sequence 13, Appl
36	428	92.4	136	4	US-10-264-049-3373	Sequence 3373, Ap
37	427	92.2	90	4	US-10-308-322-7	Sequence 7, Appli
38	427	92.2	119	4	US-10-308-322-4	Sequence 4, Appli
39	377	81.4	74	4	US-10-050-902-238	Sequence 238, App
40	377	81.4	74	4	US-10-050-898-238	Sequence 238, App
41	377	81.4	101	4	US-10-308-322-22	Sequence 22, Appl
42	377	81.4	177	4	US-10-335-394-54	Sequence 54, Appl
43	377	81.4	339	4	US-10-335-394-55	Sequence 55, Appl
44	376	81.2	70	4	US-10-050-902-239	Sequence 239, App
45	376	81.2	70	4	US-10-050-898-239	Sequence 239, App

ALIGNMENTS

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RESULT 1
US-08-927-939-22
; Sequence 22, Application US/08927939
; Publication No. US20010006640A1
; GENERAL INFORMATION:
;  APPLICANT: Grainger, David J.
;  APPLICANT: Tatalick, Lauen Marie
;  TITLE OF INVENTION: Compounds and methods to inhibit or
;  TITLE OF INVENTION: augment an inflammatory response.
;  FILE REFERENCE: 295.022US1
;  CURRENT APPLICATION NUMBER: US/08/927,939
;  CURRENT FILING DATE: 1997-09-11
;  NUMBER OF SEQ ID NOS: 83
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 22
;   LENGTH: 89
;   TYPE: PRT
;   ORGANISM: Homo sapiens
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US-08-927-939-22

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RESULT 2
US-09-953-692-4
; Sequence 4, Application US/09953692
; Patent No. US20020107195A1
; GENERAL INFORMATION:
; APPLICANT: Shalley, Gupta K.
; TITLE OF INVENTION: Method for Inducing Chemotaxis in Endothelial Cells by
; TITLE OF INVENTION: Administering Stromal Cell Derived Factor-1(
; FILE REFERENCE: P50676C1
; CURRENT APPLICATION NUMBER: US/09/953,692
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 09/358,624
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: 60/093,596
; PRIOR FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
;   LENGTH: 89
;   TYPE: PRT
;   ORGANISM: Human
US-09-953-692-4

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  Query Match             100.0%;  Score 463;  DB 3;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-47;
  Matches   89;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
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RESULT 3
US-09-953-717-4
; Sequence 4, Application US/09953717
; Patent No. US20020107196A1
; GENERAL INFORMATION:
; APPLICANT: Shalley, Gupta K.

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;  TITLE OF INVENTION: Method for Inducing Chemotaxis in Endothelial Cells by
;  TITLE OF INVENTION:  Administering Stromal Cell Derived Factor-1(
;  FILE REFERENCE: P50676D1
;  CURRENT APPLICATION NUMBER: US/09/953,717
;  CURRENT FILING DATE:  2001-09-17
;  PRIOR APPLICATION NUMBER: 09/358,624
;  PRIOR FILING DATE: 1999-07-21
;  PRIOR APPLICATION NUMBER: 60/093,596
;  PRIOR FILING DATE: 1998-07-21
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
;   LENGTH: 89
;   TYPE: PRT
;   ORGANISM: Human
US-09-953-717-4

  Query Match             100.0%;  Score 463;  DB 3;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-47;
  Matches   89;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
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RESULT 4
US-09-792-793A-32
; Sequence 32, Application US/09792793A
; Patent No. US20020168370A1
; GENERAL INFORMATION:
;  APPLICANT: McDonald, John R.
;  APPLICANT:  Coggins, Philip
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE
DAMAGE AND
;  TITLE OF INVENTION:  OTHER INFLAMMATORY CONDITIONS AND DISORDERS
;  FILE REFERENCE: 25020-601D
;  CURRENT APPLICATION NUMBER: US/09/792,793A
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
;   LENGTH: 89
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Human Chemokine Polypeptide: Stromal cell-derived
;   OTHER INFORMATION: Factor-1-Alpha (SDF-1-Alpha)
;  PUBLICATION INFORMATION:
;   JOURNAL: Genomics
;   VOLUME: 28
;   PAGES: 495-500
;   DATE: 1995
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US-09-792-793A-32

Query Match 100.0%; Score 463; DB 3; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.2e-47;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
US-10-375-209A-32
; Sequence 32, Application US/10375209A
; Publication No. US20030215421A1
; GENERAL INFORMATION:
; APPLICANT: McDonald, John R.
; APPLICANT: Coggins, Philip
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
; TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
; FILE REFERENCE: 25020-601E
; CURRENT APPLICATION NUMBER: US/10/375,209A
; CURRENT FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human Chemokine Polypeptide: Stromal cell-derived
; OTHER INFORMATION: Factor-1-Aplha (SDF-1-Alpha)
; PUBLICATION INFORMATION:
; JOURNAL: Genomics
; VOLUME: 28
; PAGES: 495-500
; DATE: 1995
US-10-375-209A-32

Query Match 100.0%; Score 463; DB 4; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.2e-47;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 6
US-10-785-230-5
; Sequence 5, Application US/10785230
; Publication No. US20040209837A1
; GENERAL INFORMATION:
; APPLICANT: KISHIMOTO, Tadamitsu
; APPLICANT: NAGASAWA, Takashi
; APPLICANT: TACHIBANA, Kazunobu
; APPLICANT: CHUGAI SEIYAKU KABUSIKI KAISHA
; TITLE OF INVENTION: Vascularization Inhibitors
; FILE REFERENCE: 46124-5042-US
; CURRENT APPLICATION NUMBER: US/10/785,230
; CURRENT FILING DATE: 2004-02-25
; PRIOR APPLICATION NUMBER: PCT/JP99/01448
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: JP10/95448
; PRIOR FILING DATE: 1998-03-24
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 5
;   LENGTH: 89
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Ligand peptide
US-10-785-230-5

  Query Match   100.0%; Score 463; DB 4; Length 89;
  Best Local Similarity   100.0%; Pred. No. 1.2e-47;
  Matches   89; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
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Db   61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89

RESULT 7
US-10-924-029-1
; Sequence 1, Application US/10924029
; Publication No. US20050020528A1
;   GENERAL INFORMATION:
;   APPLICANT: Herrmann, Stephen H.
;   Lu, Zhijian
;   McCoy, John M.
;   Swanberg, Stephen L.
;   Walker, Bruce
;   Yang, Otto
;   TITLE OF INVENTION: CHEMOKINES WITH AMINO-TERMINAL MODIFICATIONS
;   NUMBER OF SEQUENCES: 15
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Genetics Institute, Inc.
;   STREET: 87 CambridgePark Drive
;   CITY: Cambridge
;   STATE: MA

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;              COUNTRY: U.S.A.
;              ZIP: 02140
;         COMPUTER READABLE FORM:
;              MEDIUM TYPE: Floppy disk
;              COMPUTER: IBM PC compatible
;              OPERATING SYSTEM: PC-DOS/MS-DOS
;              SOFTWARE: PatentIn Release #1.0, Version #1.30
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/10/924,029
;              FILING DATE: 23-Aug-2004
;              CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: US/09/175,713
;              FILING DATE: 20-Oct-1998
;         ATTORNEY/AGENT INFORMATION:
;              NAME: Sprunger, Suzanne A.
;              REGISTRATION NUMBER: 41,323
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (617) 498-8284
;              TELEFAX: (617) 876-5851
;    INFORMATION FOR SEQ ID NO: 1:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 89 amino acids
;              TYPE: amino acid
;              STRANDEDNESS: <Unknown>
;              TOPOLOGY: linear
;         MOLECULE TYPE: protein
;         SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-924-029-1

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  Best Local Similarity   100.0%;  Pred. No. 1.2e-47;
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Db         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89


RESULT 8
US-10-985-324-4
; Sequence 4, Application US/10985324
; Publication No. US20050202019A1
; GENERAL INFORMATION:
;  APPLICANT: Northwest Biotherapeutics, Inc.
;  APPLICANT:  Murphy, Gerald P.
;  APPLICANT:  Boynton, Alton L.
;  APPLICANT:  Sehgal, Anil
;  TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC APPLICATIONS BASED ON THE
;  TITLE OF INVENTION:  ROLE OF THE CXCR-4 GENE IN TUMORIGENESIS
;  FILE REFERENCE: 20093-000600PC
;  CURRENT APPLICATION NUMBER: US/10/985,324
;  CURRENT FILING DATE:  2004-11-09
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;  PRIOR APPLICATION NUMBER: US/09/647,501
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/079,916
;  PRIOR FILING DATE: 1998-03-30
;  PRIOR APPLICATION NUMBER: 60/104,656
;  PRIOR FILING DATE: 1998-10-16
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 89
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-985-324-4

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RESULT 9
US-10-773-236-280
; Sequence 280, Application US/10773236
; Publication No. US20050208602A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et. al.
;  TITLE OF INVENTION: 89 Human Secreted Proteins
;  FILE REFERENCE: PS751P1
;  CURRENT APPLICATION NUMBER: US/10/773,236
;  CURRENT FILING DATE:  2004-02-09
;  PRIOR APPLICATION NUMBER: 60/311,085
;  PRIOR FILING DATE: 2001-08-10
;  PRIOR APPLICATION NUMBER: 60/325,209
;  PRIOR FILING DATE: 2001-09-28
;  PRIOR APPLICATION NUMBER: PCT/US02/25107
;  PRIOR FILING DATE: 2002-08-08
;  PRIOR APPLICATION NUMBER: 60/330,629
;  PRIOR FILING DATE: 2001-10-26
;  PRIOR APPLICATION NUMBER: PCT/US02/33985
;  PRIOR FILING DATE: 2002-10-24
;  PRIOR APPLICATION NUMBER: 60/331,046
;  PRIOR FILING DATE: 2001-11-07
;  PRIOR APPLICATION NUMBER: PCT/US02/35606
;  PRIOR FILING DATE: 2002-11-06
;  PRIOR APPLICATION NUMBER: 60/358,554
;  PRIOR FILING DATE: 2002-02-22
;  PRIOR APPLICATION NUMBER: PCT/US03/04819
;  PRIOR FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: 60/358,714
;  PRIOR FILING DATE: 2002-02-25
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;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 396
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 280
;   LENGTH: 89
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-773-236-280

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  Matches   89;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
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Db         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89


RESULT 10
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; Sequence 43, Application US/10921235
; Publication No. US20050214786A1
; GENERAL INFORMATION:
;  APPLICANT: Birse et al.
;  TITLE OF INVENTION: 26 Human Secreted Proteins
;  FILE REFERENCE: PS741P1
;  CURRENT APPLICATION NUMBER: US/10/921,235
;  CURRENT FILING DATE:  2004-08-19
;  PRIOR APPLICATION NUMBER: US03/04819
;  PRIOR FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: US03/04818
;  PRIOR FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: 60/358,554
;  PRIOR FILING DATE: 2002-02-22
;  PRIOR APPLICATION NUMBER: 60/358,714
;  PRIOR FILING DATE: 2002-02-25
;  NUMBER OF SEQ ID NOS: 76
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
;   LENGTH: 89
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-921-235-43

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RESULT 11
US-08-927-939-56
; Sequence 56, Application US/08927939
; Publication No. US20010006640A1
; GENERAL INFORMATION:
;  APPLICANT: Grainger, David J.
;  APPLICANT: Tatalick, Lauen Marie
;  TITLE OF INVENTION: Compounds and methods to inhibit or
;  TITLE OF INVENTION: augment an inflammatory response.
;  FILE REFERENCE: 295.022US1
;  CURRENT APPLICATION NUMBER: US/08/927,939
;  CURRENT FILING DATE: 1997-09-11
;  NUMBER OF SEQ ID NOS: 83
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 56
;   LENGTH: 93
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-08-927-939-56

  Query Match             100.0%;  Score 463;  DB 2;  Length 93;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-47;
  Matches   89;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
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Db          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

Qy         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
              ||||||||||||||||||||||||||||
Db         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89


RESULT 12
US-09-144-838-7
; Sequence 7, Application US/09144838A
; Patent No. US20020051996A1
; GENERAL INFORMATION:
;  APPLICANT: Siani, Michael A.
;  APPLICANT: Wilken, Jill
;  APPLICANT: Simon, Reyna
;  APPLICANT: Kent, Stephen B.H.
;  TITLE OF INVENTION: Modular Protein Libraries and Methods of Preparation
;  FILE REFERENCE: GRFN-020/01US
;  CURRENT APPLICATION NUMBER: US/09/144,838A
;  CURRENT FILING DATE: 1998-08-31
;  EARLIER APPLICATION NUMBER: US 60/057,620
;  EARLIER FILING DATE: 1997-09-04
;  NUMBER OF SEQ ID NOS: 54
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 93
;   TYPE: PRT
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-144-838-7

  Query Match   100.0%; Score 463; DB 3; Length 93;
  Best Local Similarity   100.0%; Pred. No. 1.3e-47;
  Matches   89; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
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Db   1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

Qy   61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
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Db   61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89

RESULT 13
US-09-919-497-95
; Sequence 95, Application US/09919497
; Patent No. US20020106662A1
; GENERAL INFORMATION:
; APPLICANT: Mutter, George L.
; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
; FILE REFERENCE: B0801/7225
; CURRENT APPLICATION NUMBER: US/09/919,497
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/221,735
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 95
;   LENGTH: 93
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-919-497-95

  Query Match   100.0%; Score 463; DB 3; Length 93;
  Best Local Similarity   100.0%; Pred. No. 1.3e-47;
  Matches   89; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
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Db   1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

Qy   61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
              |||||||||||||||||||||||||||||
Db   61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89

RESULT 14
US-09-835-107-2
; Sequence 2, Application US/09835107
; Patent No. US20020165123A1
; GENERAL INFORMATION:
; APPLICANT: Tudan, Christopher R.

```
;  APPLICANT:  Merzouk, Ahmed
;  APPLICANT:  Arab, Lakhdar
;  APPLICANT:  Saxena, Geeta
;  APPLICANT:  Eaves, Connie J.
;  APPLICANT:  Cashman, Johanne
;  APPLICANT:  Clark-Lewis
;  APPLICANT:  Salari, Hassan
;  TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
;  FILE REFERENCE: SMAR012
;  CURRENT APPLICATION NUMBER: US/09/835,107
;  CURRENT FILING DATE:  2001-08-20
;  PRIOR APPLICATION NUMBER: CA 2,305,036
;  PRIOR FILING DATE: 2000-04-12
;  PRIOR APPLICATION NUMBER: US 60/232,425
;  PRIOR FILING DATE: 2000-09-14
;  PRIOR APPLICATION NUMBER: CA 2,335,109
;  PRIOR FILING DATE: 2001-02-23
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 93
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: SDF-1 Precursor, PBSF
US-09-835-107-2

  Query Match             100.0%;  Score 463;  DB 3;  Length 93;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-47;
  Matches   89;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
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Db          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

Qy         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
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Db         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89


RESULT 15
US-09-835-107-3
; Sequence 3, Application US/09835107
; Patent No. US20020165123A1
; GENERAL INFORMATION:
;  APPLICANT: Tudan, Christopher R.
;  APPLICANT:  Merzouk, Ahmed
;  APPLICANT:  Arab, Lakhdar
;  APPLICANT:  Saxena, Geeta
;  APPLICANT:  Eaves, Connie J.
;  APPLICANT:  Cashman, Johanne
;  APPLICANT:  Clark-Lewis
;  APPLICANT:  Salari, Hassan
;  TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
;  FILE REFERENCE: SMAR012
;  CURRENT APPLICATION NUMBER: US/09/835,107
;  CURRENT FILING DATE:  2001-08-20
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;  PRIOR APPLICATION NUMBER: CA 2,305,036
;  PRIOR FILING DATE: 2000-04-12
;  PRIOR APPLICATION NUMBER: US 60/232,425
;  PRIOR FILING DATE: 2000-09-14
;  PRIOR APPLICATION NUMBER: CA 2,335,109
;  PRIOR FILING DATE: 2001-02-23
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 93
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: SDF-1 beta
US-09-835-107-3

  Query Match             100.0%;  Score 463;  DB 3;  Length 93;
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  Matches   89;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
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Db          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

Qy         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
              |||||||||||||||||||||||||||||
Db         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89


Search completed: April 26, 2006, 02:41:56
Job time : 165 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 26, 2006, 02:30:09 ; Search time 187 Seconds
(without alignments)
209.116 Million cell updates/sec

Title: US-10-785-230-5
Perfect score: 463
Sequence: 1 MNAKVVVVLVLVLTALCLSD.....VCIDPKLKWIQEYLEKALNK 89

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	463	100.0	89	2	AAR75419	Aar75419 Human SDF
2	463	100.0	89	2	AAY26177	Aay26177 Stromal c
3	463	100.0	89	2	AAY39995	Aay39995 Human SDF
4	463	100.0	89	3	AAY52508	Aay52508 Human str
5	463	100.0	89	3	AAY93603	Aay93603 A human B
6	463	100.0	89	3	AAB15791	Aab15791 Human che
7	463	100.0	89	5	ABG32978	Abg32978 Human str
8	463	100.0	89	5	ABG33066	Abg33066 Human str

9	463	100.0	89	7	ADC78236	Adc78236 Human sec
10	463	100.0	89	9	ADW64706	Adw64706 Human che
11	463	100.0	93	2	AAR75420	Aar75420 Human SDF
12	463	100.0	93	2	AAW50766	Aaw50766 Human SDF
13	463	100.0	93	2	AAY26178	Aay26178 Stromal c
14	463	100.0	93	2	AAY06725	Aay06725 Amino aci
15	463	100.0	93	3	AAB15812	Aab15812 Human che
16	463	100.0	93	5	AAU84305	Aau84305 Human end
17	463	100.0	93	5	AAB47691	Aab47691 SDF-1-bet
18	463	100.0	93	5	AAB47690	Aab47690 SDF-1 pre
19	463	100.0	93	5	AAE23952	Aae23952 Human str
20	463	100.0	93	7	ADN95190	Adn95190 Human BEC
21	463	100.0	93	7	ADP65272	Adp65272 Human str
22	463	100.0	93	8	ADN07719	Adn07719 Human str
23	463	100.0	93	8	ADP12445	Adp12445 Protein e
24	463	100.0	93	8	ADQ19853	Adq19853 Human sof
25	463	100.0	93	8	ADQ14484	Adq14484 Human che
26	463	100.0	93	8	ADR99187	Adr99187 Chemokine
27	463	100.0	93	9	ADW64707	Adw64707 Human che
28	463	100.0	93	9	ADY76111	Ady76111 Human str
29	463	100.0	93	9	ADY76110	Ady76110 Human str
30	463	100.0	93	9	ADZ21672	Adz21672 Human str
31	463	100.0	119	5	AAM48047	Aam48047 Human SDF
32	463	100.0	166	2	AAY29899	Aay29899 Human SDF
33	463	100.0	328	2	AAW76220	Aaw76220 Human che
34	454	98.1	93	8	ADN36543	Adn36543 Chemokine
35	447.5	96.7	92	8	ADN36544	Adn36544 Chemokine
36	442	95.5	89	2	AAR70994	Aar70994 Protein e
37	442	95.5	89	2	AAW50764	Aaw50764 Peptide #
38	442	95.5	89	2	AAY39996	Aay39996 Mouse SDF
39	442	95.5	89	6	AAE14828	Aae14828 Mouse str
40	442	95.5	93	2	AAW50765	Aaw50765 Peptide #
41	440	95.0	326	2	AAW76221	Aaw76221 Human che
42	435	94.0	93	5	AAM48049	Aam48049 Rat SDF-1
43	435	94.0	119	5	AAM48048	Aam48048 Rat SDF-1
44	428	92.4	136	5	ABP42241	Abp42241 Human ova
45	427	92.2	90	5	AAM48043	Aam48043 Generic S

ALIGNMENTS

RESULT 1
AAR75419
ID AAR75419 standard; protein; 89 AA.
XX
AC AAR75419;
XX
DT 15-NOV-1995 (first entry)
XX
DE Human SDF-1-alpha.
XX
KW SDF-1-alpha; stromal derived factor; hematopoietic cell;
KW inflammatory disease; infectious disease; AIDS;
KW neurodegenerative disease.
XX
OS Homo sapiens.

XX
FH Key   Location/Qualifiers
FT Peptide   1. .21
FT   /label= Sig_peptide
XX
PN CA2117953-A.
XX
PD 15-APR-1995.
XX
PF 12-OCT-1994; 94CA-02117953.
XX
PR 14-OCT-1993; 93JP-00280505.
XX
PA (ONOY) ONO PHARM CO LTD.
XX
PI Honjo T, Shirozu M, Tada H;
XX
DR WPI; 1995-207311/28.
DR N-PSDB; AAQ74088, AAQ74089.
XX
PT Polypeptide(s) used for treating diseases relating to undergrown or
PT abnormal proliferation of haematopoietic cells - e.g. inflammatory
PT diseases, infectious diseases, AIDS or neuro:degenerative diseases.
XX
PS Claim 2; Page 22; 43pp; English.
XX
CC A cDNA library prepared from human pro-B cell line FLEB14 cells was
CC screened with 32P-labeled mouse SDF-1-alpha cDNA. A positive clone
CC contained an insert of 1.9 kb (AAQ74089), including an ORF (AAQ74088)
CC encoding human SDF-1-alpha (AAR75419). Recombinant hSDF-1-alpha was
CC produced in E. coli and COS cells
XX
SQ Sequence 89 AA;

  Query Match   100.0%; Score 463; DB 2; Length 89;
  Best Local Similarity   100.0%; Pred. No. 1.4e-49;
  Matches   89; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
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Db   1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

Qy   61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
              |||||||||||||||||||||||||||||
Db   61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89

RESULT 2
AAY26177
ID AAY26177 standard; protein; 89 AA.
XX
AC AAY26177;
XX
DT 29-SEP-1999 (first entry)
XX
DE Stromal cell derived factor 1a.
XX

KW Stromal cell derived factor 1a; SDF 1a; vaccine; immune response;
KW antigen; humoral response; cell-mediated response; PCR;
KW immunostimulatory; expression plasmid vector.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1. .21
FT /note= "signal peptide"
FT Protein 22. .89
FT /label= SDF_1a
FT /note= "Stromal cell-derived factor-1a"
XX
PN WO9929728-A1.
XX
PD 17-JUN-1999.
XX
PF 11-DEC-1998; 98WO-US026291.
XX
PR 11-DEC-1997; 97US-0069281P.
XX
PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
XX
PI Gallo RC, Devico AL, Garzino-Demo A;
XX
DR WPI; 1999-385578/32.
DR N-PSDB; AAX80632.
XX
PT Methods of enhancing vaccine efficacy.
XX
PS Claim 4; Page 102; 134pp; English.
XX
CC The present sequence is stromal cell derived factor-1a. This belongs to
CC the CXC class of chemokines. This is chemotactic for mature dendritic
CC cells. The efficacy of a vaccine is enhanced by combining it with one or
CC more chemokines to enhance the immune response to an antigen. This can be
CC humoral or cell-mediated immune response. The purified chemokines,
CC fragments, derivatives or analogues are administered either concurrently
CC with one or more purified antigens against which an immune response is
CC desired or within a time period either before or after antigen
CC administration. The chemokine gene is isolated by PCR, and administered
CC by constructing an expression plasmid vector which can be expressed in a
CC coordinated manner upon introduction in a suitable cell. The vaccines are
CC immunostimulatory and can be used to treat microbial diseases especially
CC HIV
XX
SQ Sequence 89 AA;

Query Match 100.0%; Score 463; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.4e-49;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy 61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89

```
                    ||||||||||||||||||||||||||
Db          61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89


RESULT 3
AAY39995
ID   AAY39995 standard; protein; 89 AA.
XX
AC   AAY39995;
XX
DT   16-DEC-1999  (first entry)
XX
DE   Human SDF-1-alpha protein sequence.
XX
KW   CXCR4; human; neovascularisation; inhibitor; solid cancer; therapy;
KW   tissue repairing agent; vascularisation; SDF-1-alpha.
XX
OS   Homo sapiens.
XX
PN   WO9948528-A1.
XX
PD   30-SEP-1999.
XX
PF   23-MAR-1999;   99WO-JP001448.
XX
PR   24-MAR-1998;   98JP-00095448.
XX
PA   (CHUS ) CHUGAI SEIYAKU KK.
PA   (KISH/) KISHIMOTO T.
XX
PI   Kishimoto T,  Nagasawa T,  Tachibana K;
XX
DR   WPI; 1999-591042/50.
DR   N-PSDB; AAZ27612.
XX
PT   CXCR4-potentiating agents and methods useful for inhibiting
PT   neovascularization, and treating solid cancers.
XX
PS   Disclosure; Page 51-52; 63pp; Japanese.
XX
CC   This sequence is the human SDF-1-alpha protein. The invention relates to
CC   remedies inhibiting neovascularisation, remedies for solid cancer,
CC   remedies for diseases pathologically caused by neovascularisation and
CC   tissue repairing agents containing as the active ingredient a substance
CC   capable of potentiating CXCR4. Based on a finding that vascularisation is
CC   inhibited in a CXCR4 knockout mouse, it becomes possible to prepare
CC   remedies inhibiting vascularisation which contain as the active
CC   ingredient a substance capable of potentiating CXCR4, remedies for solid
CC   cancer, remedies for diseases pathologically caused by neovascularisation
CC   and tissue repairing agents containing as the active ingredient a
CC   substance capable of potentiating CXCR4. It is also possible to establish
CC   methods for treatment with the use of these remedies
XX
SQ   Sequence 89 AA;

  Query Match             100.0%;  Score 463;  DB 2;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-49;
```

```
  Matches   89;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

Qy         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
              |||||||||||||||||||||||||||||
Db         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89


RESULT 4
AAY52508
ID   AAY52508 standard; protein; 89 AA.
XX
AC   AAY52508;
XX
DT   22-FEB-2000  (first entry)
XX
DE   Human stromal cell derived factor-1 (SDF-1).
XX
KW   CXC-chemokine receptor-4; CXCR-4; stromal cell derived factor-1; SDF-1;
KW   ligand; chemotaxis; inflammation; G-protein-coupled receptor;
KW   signal transduction; CD4-independent; HIV-1; infection; proliferation;
KW   transformation; tumorigenesis; cancer; tumour; overexpression; brain;
KW   breast; colon; lung; melanoma; glioblastoma; inhibition; growth arrest;
KW   diagnosis; prognosis; marker; proliferative disorders; antisense;
KW   therapy; treatment; premalignant condition; hypertrophy;
KW   degenerative disorder; Parkinson's disease; Alzheimer's disease;
KW   growth deficiency; hypoproliferative disorder; physical trauma; lesion;
KW   ischaemia; wound.
XX
OS   Homo sapiens.
XX
PN   WO9950461-A1.
XX
PD   07-OCT-1999.
XX
PF   29-MAR-1999;   99WO-US007431.
XX
PR   30-MAR-1998;   98US-0079916P.
PR   16-OCT-1998;   98US-0104656P.
XX
PA   (NWBI-) NORTHWEST BIOTHERAPEUTICS INC.
XX
PI   Murphy GP,  Boynton AL,  Sehgal A;
XX
DR   WPI; 2000-052634/04.
DR   N-PSDB; AAZ38554.
XX
PT   Use of CXCR-4 and SDF-1 as markers for diagnosis and treatment of e.g.
PT   tumors, degenerative disorders, growth deficiencies, hyper- and
PT   hypoproliferative disorders, physical trauma, lesions and wounds.
XX
PS   Disclosure; Fig 15; 138pp; English.
XX
CC   This sequence represents stromal cell derived factor-1 (SDF-1) cDNA. SDF-
```

CC 1 is the ligand for CXC-chemokine receptor-4 (CXCR-4, AAY52507).
CC Chemokine receptors play an important role in the chemotaxis of T-cells
CC and phagocytic cells to areas of inflammation. CXCR-4 is a member of the
CC G-protein-coupled receptor family, which is involved in signal
CC transduction. CXCR-4 also mediates CD4-independent infection by HIV-1.
CC CXCR-4 has now been found to have a role in the aberrant proliferative
CC behaviour of a number of cell types, including numerous primary tumours
CC and derived cell lines. CXCR-4 is involved in cell transformation and
CC tumorigenesis, particularly in brain, breast and colon tumours. It was
CC found to be overexpressed in several brain tumour derived cell lines and
CC primary brain tumour tissues, breast tumour tissues, colorectal
CC adenocarcinoma, lung carcinoma and melanoma cell lines. CXCR-4 expression
CC was required for the continuous proliferation of glioblastoma cancer
CC cells, and inhibition of its gene function resulted in growth arrest.
CC Conversely, overexpression resulted in enhanced and rapid cellular
CC proliferation. CXCR-4 and SDF-1 can be used as markers for the diagnosis
CC and prognosis of cell proliferative disorders, and antisense
CC oligonucleotides complementary to at least a portion of an RNA transcript
CC of a CXCR-4 gene can be used to inhibit hyperproliferation of a tumour
CC cell. Agents that inhibit CXCR-4 function can be used for treating or
CC preventing a disease or disorder involving cell overproliferation, e.g.,
CC brain cancer, breast cancer, colon cancer, prostate cancer and B cell
CC lymphoma, and also premalignant conditions, benign tumours,
CC hyperproliferative disorders, and benign dysproliferative disorders. They
CC can also be used for treating e.g., cirrhosis of the liver, keloid
CC formation, psoriasis, benign tumors, fibrocystic conditions and tissue
CC hypertrophy. Compounds that promote CXCR-4 function can also be used for
CC preventing or treating a disease or disorder involving a deficiency in
CC cell proliferation, or treating a condition where cell proliferation
CC would be desirable. Such diseases include degenerative disorders (e.g.,
CC Parkinson's disease, Alzheimer's disease), growth deficiencies,
CC hypoproliferative disorders, physical trauma, lesions (e.g., those caused
CC by ischaemia), and wounds
XX
SQ Sequence 89 AA;

Query Match 100.0%; Score 463; DB 3; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.4e-49;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

Qy         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
              |||||||||||||||||||||||||||||
Db         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
```

RESULT 5
AAY93603
ID AAY93603 standard; protein; 89 AA.
XX
AC AAY93603;
XX
DT 25-SEP-2000 (first entry)
XX

DE A human B-cell stimulating factor homologue (SDF1a).
XX
KW Differentially expressed human gene; cardiac disease; kidney disease;
KW inflammatory disease; I-8U; prostacyclin-stimulating factor; isf-2;
KW tissue specific mRNA; insulin-like growth factor binding protein 6;
KW OSF-1; gas-1; YMP; BTG2; pre-B cell stimulating factor homologue; SDF1a;
KW peripheral benzodiazepine receptor; annexin II cellular ligand; p11;
KW congenital heart failure; dilated congestive cardiomyopathy;
KW hypertrophic cardiomyopathy; restrictive cardiomyopathy;
KW mitral valve disease; aortic valve disease; tricuspid valve disease;
KW angina pectoris; myocardial infarction; cardiac arrhythmia;
KW pulmonary hypertension; arterial hypertension; renovascular hypertension;
KW arteriosclerosis; atherosclerosis; cardiac tumour.
XX
OS Homo sapiens.
XX
PN WO200035473-A2.
XX
PD 22-JUN-2000.
XX
PF 15-DEC-1999; 99WO-US029941.
XX
PR 18-DEC-1998; 98US-0113008P.
XX
PA (SCIO-) SCIOS INC.
XX
PI Stanton LW, White RT, Damm DL, Lewicki JA, Joly A, Schreiner GF;
XX
DR WPI; 2000-451904/39.
DR N-PSDB; AAA46677.
XX
PT Preventing, diagnosing and treating cardiac, kidney and inflammatory
PT disorders using cardiac genes that are differentially expressed in
PT disease states such as cardiac arrhythmia and arteriosclerosis.
XX
PS Disclosure; Fig 8J; 170pp; English.
XX
CC AAY93594-Y93605 are encoded by differentially expressed human genes,
CC associated with disease states and disorders. The specification describes
CC methods preventing, diagnosing and treating cardiac, kidney and
CC inflammatory diseases associated with inappropriate expression of
CC differentially expressed cardiac, kidney and inflammatory genes (e.g.
CC AAA46668-79). These genes include I-8U, prostacyclin-stimulating factor,
CC isf-2, tissue specific mRNA, insulin-like growth factor binding protein
CC 6, OSF-1, gas-1, YMP, BTG2, pre-B cell stimulating factor homologue
CC (SDF1a), peripheral benzodiazepine receptor, and cellular ligand of
CC annexin II (p11), respectively. These diseases include congenital heart
CC failure, dilated congestive cardiomyopathy, hypertrophic cardiomyopathy,
CC restrictive cardiomyopathy, mitral valve disease, aortic valve disease,
CC tricuspid valve disease, angina pectoris, myocardial infarction, cardiac
CC arrhythmia, pulmonary hypertension, arterial hypertension, renovascular
CC hypertension, arteriosclerosis, atherosclerosis and/or cardiac tumours
XX
SQ Sequence 89 AA;

Query Match 100.0%; Score 463; DB 3; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.4e-49;

```
  Matches   89;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

Qy         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
              |||||||||||||||||||||||||||||
Db         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89


RESULT 6
AAB15791
ID   AAB15791 standard; protein; 89 AA.
XX
AC   AAB15791;
XX
DT   17-JAN-2001  (first entry)
XX
DE   Human chemokine SDF1alpha SEQ ID NO: 22.
XX
KW   Macrophage recruitment; chemokine derivative; MCP-1; osteoporosis;
KW   monocyte chemoattractant protein-1; inflammation; atherosclerosis; HIV;
KW   AIDS; stroke; psoriasis; autoimmune disease; hypertension; endotoxaemia;
KW   basophil-mediated disease; myocardial infarction; acute ischaemia;
KW   rheumatoid arthritis; contraception.
XX
OS   Homo sapiens.
XX
PN   WO200042071-A2.
XX
PD   20-JUL-2000.
XX
PF   12-JAN-2000; 2000WO-US000821.
XX
PR   12-JAN-1999;   99US-00229071.
PR   17-MAR-1999;   99US-00271192.
PR   01-DEC-1999;   99US-00452406.
XX
PA   (NEOR-) NEORX CORP.
XX
PI   Grainger DJ,  Tatalick LM;
XX
DR   WPI; 2000-499101/44.
DR   N-PSDB; AAA74883.
XX
PT   New peptide 3, amide and heterocyclic compounds and saccharide conjugates
PT   used for inhibiting chemokine induced activity and for treating e.g.
PT   stroke, vascular diseases, autoimmune diseases and tumor growth.
XX
PS   Example 1; Page 134; 387pp; English.
XX
CC   The present invention concerns the identification of a number of
CC   chemokines which can be used to produce derivatives, agonists and
CC   antagonists which are then useful in disease treatment. The chemokines
CC   include sequences AAB15785-B15794, AAB15803-B15813 and AAB15831-B15848.
CC   These chemokine derivatives can be used to treat diseases such as
```

CC autoimmune diseases, atherosclerosis, osteoporosis, HIV infection and
CC AIDS, psoriasis, inflammatory diseases, hypertension, basophil-mediated
CC diseases, endotoxaemia, myocardial infarction, acute ischaemia and
CC rheumatoid arthritis, and can be used to prevent strokes and as
CC contraceptives. The coding sequences for the chemokines can be used in
CC gene therapy for the same diseases, as well as in the production of
CC animal models
XX
SQ Sequence 89 AA;

Query Match 100.0%; Score 463; DB 3; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.4e-49;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

Qy         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
              |||||||||||||||||||||||||||||
Db         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
```

RESULT 7
ABG32978
ID ABG32978 standard; protein; 89 AA.
XX
AC ABG32978;
XX
DT 02-DEC-2002 (first entry)
XX
DE Human stromal cell derived factor 1-alpha (SDF 1-alpha).
XX
KW CXC chemokine receptor 4; CXCR4; chemotaxis induction; SDF1alpha;
KW stromal cell-derived factor 1alpha; angiogenesis; atherosclerosis;
KW restenosis; ischaemic stroke; spinal cord injury; infection; ulcer;
KW human immunodeficiency virus; HIV; acquired immunodeficiency syndrome;
KW AIDS; pain; cancer; benign prostatic hypertrophy; diabetes; obesity;
KW anorexia; bulimia; asthma; Parkinson's disease; acute heart failure;
KW hypotension; hypertension; urinary retention; osteoporosis; stroke;
KW anginal pectoris; myocardial infarction; benign prostatic hypertrophy;
KW migraine; vomiting; psychotic disorder; neurological disorder; anxiety;
KW schizophrenia; dyskinesia; Huntingdon's disease; restenosis;
KW inflammatory disease; rheumatoid arthritis; diabetic retinopathy;
KW inflammatory bowel disease; atherosclerosis; Alzheimer's disease;
KW congestive heart failure; cardiac remodeling; angiogenic diseases;
KW solid tumour; Kaposi Sarcoma; human.
XX
OS Homo sapiens.
XX
PN US2002107195-A1.
XX
PD 08-AUG-2002.
XX
PF 17-SEP-2001; 2001US-00953692.
XX
PR 21-JUL-1998; 98US-0093596P.

PR 21-JUL-1999; 99US-00358624.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Gupta SK;
XX
DR WPI; 2002-697879/75.
DR N-PSDB; ABS53989.
XX
PT Inducing chemotaxis of endothelial cells, useful for regulating
PT angiogenesis, e.g. for treating cancer, comprises treatment with stromal
PT cell-derived factor 1 alpha.
XX
PS Claim 1; Fig 2; 26pp; English.
XX
CC The invention describes a method of inducing chemotaxis of endothelial
CC cells by treatment with stromal cell-derived factor 1alpha (SDF1a). The
CC method is used for stimulating EC chemotaxis, and thus angiogenesis, and
CC is used for treating atherosclerosis, restenosis, ischaemic stroke and
CC spinal cord injury. Inhibition of this process is useful in treatment and
CC prevention of a very wide range of diseases, such as, infection (by
CC bacteria, fungi, protozoa or viruses such as human immunodeficiency virus
CC (HIV) and acquired immunodeficiency syndrome (AIDS)), pain, cancer and
CC benign prostatic hypertrophy, diabetes, obesity, anorexia, bulimia,
CC asthma, Parkinson's disease, acute heart failure, hypotension,
CC hypertension, urinary retention, osteoporosis, anginal pectoris,
CC myocardial infarction, stroke, ulcers, benign prostatic hypertrophy,
CC migraine, vomiting, psychotic and neurological disorders (e.g. anxiety,
CC schizophrenia) and dyskinesias (e.g. Huntingdon's disease), inflammatory
CC diseases, rheumatoid arthritis, diabetic retinopathy, inflammatory bowel
CC disease, atherosclerosis, restenosis, Alzheimer's disease, congestive
CC heart failure, cardiac remodeling, angiogenic diseases, solid tumours,
CC and Kaposi Sarcoma. This is the amino acid sequence of human stromal cell
CC derived factor 1-alpha (SDF 1-alpha)
XX
SQ Sequence 89 AA;

Query Match 100.0%; Score 463; DB 5; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.4e-49;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

Qy         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
              |||||||||||||||||||||||||||||
Db         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
```

RESULT 8
ABG33066
ID ABG33066 standard; protein; 89 AA.
XX
AC ABG33066;
XX
DT 28-NOV-2002 (first entry)

XX
DE Human stromal cell derived factor-1a (SDF-1alpha).
XX
KW Chemotaxis; endothelial cell; EC; angiogenesis; atherosclerosis;
KW restenosis; ischaemic stroke; spinal cord injury; infection; bacteria;
KW fungi; protozoa; virus; pain; cancer; benign prostatic hypertrophy;
KW diabetes; obesity; anorexia; bulimia; asthma; allergy; hypertension;
KW Parkinson's disease; acute heart failure; hypotension; urinary retention;
KW osteoporosis; angina pectoris; myocardial infarction; stroke; dyskinesia;
KW migraine; vomiting; psychotic disorder; neurological disorder; ulcer;
KW inflammatory disorder; rheumatoid arthritis; diabetic retinopathy;
KW inflammatory bowel disease; atherosclerosis; restenosis; Kaposi sarcoma;
KW Alzheimer's disease; congestive heart failure; cardiac remodelling;
KW angiogenic disease; solid tumour; human; stromal cell derived factor-1a;
KW SDF-1alpha.
XX
OS Homo sapiens.
XX
PN US2002107196-A1.
XX
PD 08-AUG-2002.
XX
PF 17-SEP-2001; 2001US-00953717.
XX
PR 21-JUL-1998; 98US-0093596P.
PR 21-JUL-1999; 99US-00358624.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Gupta SK;
XX
DR WPI; 2002-706230/76.
DR N-PSDB; ABS53747.
XX
PT Inducing chemotaxis of endothelial cells, useful for regulating
PT angiogenesis, e.g. for treating cancer, comprises treatment with stromal
PT cell-derived factor 1 alpha.
XX
PS Claim 1; Fig 2; 26pp; English.
XX
CC The present invention relates to a new method for inducing chemotaxis of
CC endothelial cells (EC). The method of the invention involves treatment
CC with a stromal cell-derived factor 1a (SDF1alpha). The method is used for
CC stimulating EC chemotaxis, and thus angiogenesis, and is used for
CC treating atherosclerosis, restenosis, ischaemic stroke and spinal cord
CC injury, while inhibition of this process is useful in treatment and
CC prevention of a very wide range of diseases, e.g. infection (by bacteria,
CC fungi, protozoa or viruses), pain, cancer and benign prostatic
CC hypertrophy, diabetes, obesity, anorexia, bulimia, asthma, allergies,
CC Parkinson's disease, acute heart failure, hypotension, hypertension,
CC urinary retention, osteoporosis, angina pectoris, myocardial infarction,
CC stroke, ulcers, migraine, vomiting, psychotic and neurological disorders
CC and dyskinesias, inflammatory disorders, rheumatoid arthritis, diabetic
CC retinopathy, inflammatory bowel disease, atherosclerosis, restenosis,
CC Alzheimer's disease, congestive heart failure, cardiac remodelling,
CC angiogenic diseases, solid tumours, and Kaposi sarcoma. The present amino
CC acid sequence represents the human stromal cell derived factor-1a (SDF-

CC 1alpha) protein of the invention
XX
SQ Sequence 89 AA;

Query Match 100.0%; Score 463; DB 5; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.4e-49;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

Qy         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
              |||||||||||||||||||||||||||||
Db         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
```

RESULT 9
ADC78236
ID ADC78236 standard; protein; 89 AA.
XX
AC ADC78236;
XX
DT 01-JAN-2004 (first entry)
XX
DE Human secreted protein SEQ ID NO:43.
XX
KW human; secreted protein; neuroprotective; nootropic; antiparkinsonian;
KW immunosuppressive; dermatological; antiinflammatory; antirheumatic;
KW antiarthritic; antithyroid; antianaemic; antidiabetic; hepatotropic;
KW antiasthmatic; antiallergic; nephrotropic; antiarteriosclerotic;
KW cardiant; anti-HIV; virucide; antibacterial; fungicide; gynaecological;
KW cytostatic; gene therapy; neural disorder; immune system disorder;
KW muscular disorder; reproductive disorder; gastrointestinal disorder;
KW pulmonary disorder; cardiovascular disorder; renal disorder;
KW proliferative disorders; cancer; systemic lupus erythematosus;
KW rheumatoid arthritis; multiple sclerosis; thyroiditis; anaemia;
KW Grave's disease; diabetes; hepatitis; asthma; allergy; nephritis;
KW Parkinson's disease; Alzheimer's disease; atherosclerosis;
KW myocardial infarction; AIDS; infection.
XX
OS Homo sapiens.
XX
PN WO2003072761-A1.
XX
PD 04-SEP-2003.
XX
PF 20-FEB-2003; 2003WO-US004819.
XX
PR 22-FEB-2002; 2002US-0358554P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Birse CE, Komatsoulis G, Choi GH, Olsen H, Ni J, Baker KP;
XX
DR WPI; 2003-721771/68.
DR P-PSDB; ADC78210.

XX
PT New secreted polypeptides and nucleic acid molecules for diagnosing,
PT preventing or treating diseases associated with aberrant expression or
PT activity of the polypeptide, e.g. cancer, asthma, AIDS, Parkinson's
PT disease or diabetes.
XX
PS Claim 11; SEQ ID NO 43; 572pp; English.
XX
CC The present invention describes an isolated nucleic acid molecule (I)
CC encoding a human secreted protein. Also described: (1) a recombinant
CC vector comprising (I); (2) making a recombinant host cell comprising (I);
CC (3) an isolated polypeptide (II) comprising a sequence that is at least
CC 95% identical to the polypeptide or its fragment, domain, epitope,
CC (allelic) variant or homologue encoded by (I); (4) an isolated antibody
CC that binds specifically to (II); (5) a recombinant host cell produced by
CC the above method and that expresses (II); (6) making an isolated
CC polypeptide; (7) preventing, treating or ameliorating a medical condition
CC ; (8) diagnosing a pathological condition or a susceptibility to a
CC pathological condition in a subject; (9) identifying a binding partner to
CC the above polypeptide; (10) identifying an activity in a biological assay
CC ; and (11) the product produced by method (9). (I) and (II) have
CC neuroprotective, nootropic, antiparkinsonian, immunosuppressive,
CC dermatological, antiinflammatory, antirheumatic, antiarthritic,
CC antithyroid, antianaemic, antidiabetic, hepatotropic, antiasthmatic,
CC antiallergic, nephrotropic, antiarteriosclerotic, cardiant, anti-HIV,
CC virucide, antibacterial, fungicide, gynaecological and cytostatic
CC activities, and can be used in gene therapy. The nucleic acid molecule
CC (I) and polypeptide (II) can be used in diagnosing, preventing,
CC prognosing or treating diseases or disorders associated with aberrant
CC expression and/or activity of the above polypeptide, such as neural
CC disorders, immune system disorders, muscular disorders, reproductive
CC disorders, gastrointestinal disorders, pulmonary disorders,
CC cardiovascular disorders, renal disorders, proliferative disorders and/or
CC cancers. In particular, these diseases are systemic lupus erythematosus,
CC rheumatoid arthritis, multiple sclerosis, thyroiditis, anaemia, Grave's
CC disease, diabetes, hepatitis, asthma, allergies, nephritis, Parkinson's
CC disease, Alzheimer's disease, atherosclerosis, myocardial infarction,
CC AIDS, or infections. The methods may be used for identifying agonists and
CC antagonists of the polynucleotide and polypeptide. The present sequence
CC represents a human secreted protein from the present invention.
XX
SQ Sequence 89 AA;

Query Match 100.0%; Score 463; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.4e-49;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

Qy         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
              |||||||||||||||||||||||||||||
Db         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
```

RESULT 10

ADW64706
ID ADW64706 standard; protein; 89 AA.
XX
AC ADW64706;
XX
DT 07-APR-2005 (first entry)
XX
DE Human chemokine SDF-1alpha protein sequence SeqID1.
XX
KW chemokine; virucide; anti-HIV; antiinflammatory; immunosuppressive;
KW HIV infection; inflammation; autoimmune disease; veterinary;
KW gene therapy; SDF-1alpha.
XX
OS Homo sapiens.
XX
PN US2005020528-A1.
XX
PD 27-JAN-2005.
XX
PF 23-AUG-2004; 2004US-00924029.
XX
PR 28-FEB-1997; 97US-00808720.
PR 22-OCT-1997; 97US-0113672P.
PR 20-OCT-1998; 98US-00175713.
XX
PA (HERR/) HERRMANN S H.
PA (LUZZ/) LU Z.
PA (MCCO/) MCCOY J M.
PA (SWAN/) SWANBERG S L.
PA (WALK/) WALKER B.
PA (YANG/) YANG O.
XX
PI Herrmann SH, Lu Z, Mccoy JM, Swanberg SL, Walker B, Yang O;
XX
DR WPI; 2005-100856/11.
DR N-PSDB; ADW64708.
XX
PT New composition comprises isolated polynucleotide encoding an amino-
PT terminal-modified chemokine or an amino-terminal-modified chemokine,
PT useful for preventing, treating, or ameliorating HIV infection,
PT inflammatory, or autoimmune condition.
XX
PS Example 1; SEQ ID NO 1; 29pp; English.
XX
CC This invention relates to a novel composition which comprises an isolated
CC polynucleotide encoding an amino-terminal-modified chemokine or comprises
CC an amino-terminal-modified chemokine. The invention may be useful for the
CC production of compounds with a virucide, anti-HIV, antiinflammatory or
CC immunosuppressive activity. The composition is useful for preventing,
CC treating, or ameliorating an HIV infection, an inflammatory condition, or
CC an autoimmune condition. The composition is also useful for veterinary
CC applications. The amino-terminal-modified chemokine are useful as tolls
CC for identifying cells expressing receptor for the chemokine, or for
CC studying binding of chemokine to isolated receptor molecules. They can
CC also be used as vaccine adjuvants or to affect the chemotactic
CC recruitment of migratory cells. The polynucleotides can also be used in
CC gene therapy. The amino-terminal-modified chemokine is a more successful

CC inhibitor of HIV infection than the corresponding unmodified chemokine.
CC The present sequence is that of wild-type human chemokine SDF-1alpha
CC which was used during the development of the composition of the
CC invention.
XX
SQ Sequence 89 AA;

Query Match 100.0%; Score 463; DB 9; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.4e-49;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

Qy         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
              |||||||||||||||||||||||||||||
Db         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
```

RESULT 11
AAR75420
ID AAR75420 standard; protein; 93 AA.
XX
AC AAR75420;
XX
DT 15-NOV-1995 (first entry)
XX
DE Human SDF-1-beta.
XX
KW SDF-1-beta; stromal derived factor; hematopoietic cell;
KW inflammatory disease; infectious disease; AIDS;
KW neurodegenerative disease.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1. .21
FT /label= Sig_peptide
XX
PN CA2117953-A.
XX
PD 15-APR-1995.
XX
PF 12-OCT-1994; 94CA-02117953.
XX
PR 14-OCT-1993; 93JP-00280505.
XX
PA (ONOY) ONO PHARM CO LTD.
XX
PI Honjo T, Shirozu M, Tada H;
XX
DR WPI; 1995-207311/28.
DR N-PSDB; AAQ74090, AAQ74091.
XX
PT Polypeptide(s) used for treating diseases relating to undergrown or
PT abnormal proliferation of haematopoietic cells - e.g. inflammatory

PT diseases, infectious diseases, AIDS or neuro:degenerative diseases.
XX
PS Claim 12; Page 26-27; 43pp; English.
XX
CC A cDNA library prepared from human pro-B cell line FLEB14 cells was
CC screened with 32P-labeled mouse SDF-1-alpha cDNA. A positive clone
CC contained an insert of 3.5 kb (AAQ74091), including an ORF (AAQ74090)
CC encoding human SDF-1-beta (AAR75420). Recombinant hSDF-1-beta was
CC produced in E. coli and COS cells
XX
SQ Sequence 93 AA;

Query Match 100.0%; Score 463; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 1.5e-49;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

Qy         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
              |||||||||||||||||||||||||||||
Db         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
```

RESULT 12
AAW50766
ID AAW50766 standard; peptide; 93 AA.
XX
AC AAW50766;
XX
DT 27-JUL-1998 (first entry)
XX
DE Human SDF-1 which is useful for treating HIV.
XX
KW Stromal cell-derived chemokine; SDF-1; human immunodeficiency virus; HIV;
KW CXCR4 receptor; leukocyte-expressed transmembrane domain receptor.
XX
OS Homo sapiens.
XX
PN FR2751658-A1.
XX
PD 30-JAN-1998.
XX
PF 26-JUL-1996; 96FR-00009477.
XX
PR 26-JUL-1996; 96FR-00009477.
XX
PA (INSP) INST PASTEUR.
XX
PI Arenzana SF, Virelizier JL, Baggiolini M, Moser B, Clark LI;
XX
DR WPI; 1998-123039/12.
DR P-PSDB; AAV07076.
XX
PT Human stromal cell-derived chemokine, SDF-1 - useful for treating human
PT immunodeficiency virus infection.

XX
PS Claim 4; Fig 5; 48pp; French.
XX
CC The invention relates to peptides which bind to a cellular receptor for
CC CXC chemokines, namely the CXCR4 receptor (also known as leukocyte-
CC expressed transmembrane domain receptor), especially where the peptide is
CC human chemokine SDF-1. The peptide can be used to treat or prevent HIV
CC infections, optionally together with reverse transcriptase inhibitors,
CC viral protease inhibitors, soluble CD4 receptors, CD4 receptor
CC antagonists, immunotherapy agents, agents for treating HIV- associated
CC opportunistic infections and/or other CXC or CC chemokines, especially
CC RANTES, MIP1- alpha , MIP1- beta or MCP1. The peptide can be used to
CC detect anti-SDF-1 antibodies in biological fluids. This sequence
CC represents human SDF-1
XX
SQ Sequence 93 AA;

Query Match 100.0%; Score 463; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 1.5e-49;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

Qy         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
              |||||||||||||||||||||||||||||
Db         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
```

RESULT 13
AAY26178
ID AAY26178 standard; protein; 93 AA.
XX
AC AAY26178;
XX
DT 29-SEP-1999 (first entry)
XX
DE Stromal cell derived factor 1b.
XX
KW Stromal cell derived factor 1b; SDF 1b; vaccine; immune response;
KW antigen; humoral response; cell-mediated response; PCR;
KW immunostimulatory; expression plasmid vector.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1. .21
FT /note= "Signal peptide"
FT Protein 22. .93
FT /label= SDF_1b
FT /note= "Stromal cell-derived factor 1b"
XX
PN WO9929728-A1.
XX
PD 17-JUN-1999.
XX

PF 11-DEC-1998; 98WO-US026291.
XX
PR 11-DEC-1997; 97US-0069281P.
XX
PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
XX
PI Gallo RC, Devico AL, Garzino-Demo A;
XX
DR WPI; 1999-385578/32.
DR N-PSDB; AAX80633.
XX
PT Methods of enhancing vaccine efficacy.
XX
PS Claim 4; Page 103; 134pp; English.
XX
CC The present sequence is stromal cell derived factor-1b. This belongs to
CC the CXC class of chemokines.This is chemotactic for mature dendritic
CC cells. The efficacy of a vaccine is enhanced by combining it with one or
CC more chemokines to enhance the immune response to an antigen. This can be
CC humoral or cell-mediated immune response. The purified chemokines,
CC fragments, derivatives or analogues are administered either concurrently
CC with one or more purified antigens against which an immune response is
CC desired or within a time period either before or after antigen
CC administration. The chemokine gene is isolated by PCR, and administered
CC by constructing an expression plasmid vector which can be expressed in a
CC coordinated manner upon introduction in a suitable cell. The vaccines are
CC immunostimulatory and can be used to treat microbial diseases especially
CC HIV
XX
SQ Sequence 93 AA;

  Query Match   100.0%; Score 463; DB 2; Length 93;
  Best Local Similarity   100.0%; Pred. No. 1.5e-49;
  Matches   89; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

Qy   61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
              |||||||||||||||||||||||||||||
Db   61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89

RESULT 14
AAY06725
ID AAY06725 standard; protein; 93 AA.
XX
AC AAY06725;
XX
DT 18-JUN-1999 (first entry)
XX
DE Amino acid sequence of native SDF-1 alpha.
XX
KW Chemokine; cross-over protein; pharmaceutical; inflammatory; AIDS; viral;
KW infectious disease; hematopoiesis; chemoprotection; asthma; RANTES; vMIP;
KW allergic rhinitis; atopic dermatitis; rheumatoid arthritis; SDF-1; MPAV;

KW stromal cell derived factor 1; Macrophage Inflammatory protein.
XX
OS Homo sapiens.
XX
PN WO9911655-A1.
XX
PD 11-MAR-1999.
XX
PF 31-AUG-1998; 98WO-US018096.
XX
PR 04-SEP-1997; 97US-0057620P.
XX
PA (GRYP-) GRYPHON SCI.
XX
PI Kent SBH, Siani MA, Simon R, Wilken J;
XX
DR WPI; 1999-205128/17.
XX
PT New cross-over proteins for treatment of inflammation and infections e.g.
PT AIDS - prepared by ligation of two functional protein modules derived
PT from two different parent molecules.
XX
PS Example 4; Page 41; 75pp; English.
XX
CC The invention relates to a cross-over protein produced by chemical
CC ligation of at least two functional protein modules derived from at least
CC two parent protein molecules. The cross-over proteins can be used in
CC pharmaceutical compositions for therapy of inflammatory and infectious
CC diseases including AIDS, and for indications of hematopoiesis and
CC chemoprotection. They are also useful for treatment of asthma, allergic
CC rhinitis, atopic dermatitis and rheumatoid arthritis. A library
CC comprising a collection of cross-over proteins is useful for screening
CC for cross-over proteins that are receptor ligands. The libraries comprise
CC functionally diverse compounds therefore improving the drug discovery
CC process. The proteins and libraries are exemplified by the preparation of
CC cross-over chemokines comprising various combinations of peptide segments
CC derived from RANTES, SDF-1 (stromal cell derived factor 1), vMIP (viral
CC Macrophage Inflammatory protein) and other such chemokines. The present
CC sequence represents a native amino acid fragment of SDF-1 alpha
XX
SQ Sequence 93 AA;

Query Match 100.0%; Score 463; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 1.5e-49;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

Qy         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
              |||||||||||||||||||||||||||||
Db         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
```

RESULT 15
AAB15812

ID AAB15812 standard; protein; 93 AA.
XX
AC AAB15812;
XX
DT 17-JAN-2001 (first entry)
XX
DE Human chemokine SDF1beta SEQ ID NO: 56.
XX
KW Macrophage recruitment; chemokine derivative; MCP-1; osteoporosis;
KW monocyte chemoattractant protein-1; inflammation; atherosclerosis; HIV;
KW AIDS; stroke; psoriasis; autoimmune disease; hypertension; endotoxaemia;
KW basophil-mediated disease; myocardial infarction; acute ischaemia;
KW rheumatoid arthritis; contraception.
XX
OS Homo sapiens.
XX
PN WO200042071-A2.
XX
PD 20-JUL-2000.
XX
PF 12-JAN-2000; 2000WO-US000821.
XX
PR 12-JAN-1999; 99US-00229071.
PR 17-MAR-1999; 99US-00271192.
PR 01-DEC-1999; 99US-00452406.
XX
PA (NEOR-) NEORX CORP.
XX
PI Grainger DJ, Tatalick LM;
XX
DR WPI; 2000-499101/44.
DR N-PSDB; AAA74869.
XX
PT New peptide 3, amide and heterocyclic compounds and saccharide conjugates
PT used for inhibiting chemokine induced activity and for treating e.g.
PT stroke, vascular diseases, autoimmune diseases and tumor growth.
XX
PS Disclosure; Page 366; 387pp; English.
XX
CC The present invention concerns the identification of a number of
CC chemokines which can be used to produce derivatives, agonists and
CC antagonists which are then useful in disease treatment. The chemokines
CC include sequences AAB15785-B15794, AAB15803-B15813 and AAB15831-B15848.
CC These chemokine derivatives can be used to treat diseases such as
CC autoimmune diseases, atherosclerosis, osteoporosis, HIV infection and
CC AIDS, psoriasis, inflammatory diseases, hypertension, basophil-mediated
CC diseases, endotoxaemia, myocardial infarction, acute ischaemia and
CC rheumatoid arthritis, and can be used to prevent strokes and as
CC contraceptives. The coding sequences for the chemokines can be used in
CC gene therapy for the same diseases, as well as in the production of
CC animal models
XX
SQ Sequence 93 AA;

  Query Match   100.0%; Score 463; DB 3; Length 93;
  Best Local Similarity   100.0%; Pred. No. 1.5e-49;
  Matches   89; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

Qy         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
              |||||||||||||||||||||||||||||
Db         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
```

Search completed: April 26, 2006, 02:33:39
Job time : 190 secs

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 26, 2006, 02:33:59 ; Search time 38 Seconds
(without alignments)
225.350 Million cell updates/sec

Title: US-10-785-230-5
Perfect score: 463
Sequence: 1 MNAKVVVVLVLVLTALCLSD.....VCIDPKLKWIQEYLEKALNK 89

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	463	100.0	93	2	G01540	cytokine SDF-1-bet
2	442	95.5	89	2	I53416	interleukin-8 homo
3	442	95.5	89	2	A53497	pre-B-cell growth-
4	442	95.5	93	2	I81182	cytokine - mouse
5	113.5	24.5	101	2	I48148	Neutrophil attract
6	113	24.4	99	2	A37034	interleukin-8 prec
7	112.5	24.3	96	2	A32954	gro-alpha precurso
8	111	24.0	95	2	JN0841	interleukin-8 - do
9	111	24.0	98	2	I59277	Mob-1 - rat
10	110	23.8	103	2	A26736	transformation-ind
11	108	23.3	103	2	I50417	RSV-induced protei
12	107	23.1	101	2	S42496	interleukin-8 prec
13	106.5	23.0	91	1	A28815	monocyte chemoattr

14	106.5	23.0	91	1	A46539	monocyte chemoattr
15	106.5	23.0	101	2	B28414	growth-regulated p
16	104.5	22.6	100	2	JH0200	macrophage inflamm
17	103.5	22.4	107	2	B38290	GRO-gamma precurso
18	102.5	22.1	100	2	I55614	macrophage inflamm
19	102.5	22.1	100	2	S21467	macrophage inflamm
20	102	22.0	101	2	I46871	interleukin-8 - ra
21	101.5	21.9	96	2	JN0572	neutrophil chemo-a
22	100.5	21.7	107	2	JH0281	macrophage inflamm
23	99	21.4	98	2	A45492	IP-10 precursor -
24	98.5	21.3	120	2	JE0177	lymphocyte and mon
25	98	21.2	103	2	A53096	interleukin-8 prec
26	97	21.0	119	2	S42881	platelet basic pro
27	96.5	20.8	107	2	A28414	melanoma growth-st
28	96.5	20.8	120	2	I48147	monocyte chemoattr
29	95	20.5	148	1	S07723	immediate-early se
30	94.5	20.4	92	2	I52322	macrophage inflamm
31	94.5	20.4	128	1	TGHU	beta-thromboglobul
32	93	20.1	109	2	A54678	monocyte chemotact
33	87.5	18.9	126	2	A35766	platelet factor 4,
34	86	18.6	98	1	TGHUGI	interferon gamma-i
35	86	18.6	100	2	S46198	cytokine-induced n
36	84.5	18.3	148	1	A30209	PDGF-inducible JE
37	84	18.1	75	2	A54188	granulocyte chemot
38	83.5	18.0	114	2	A55010	neutrophil-activat
39	83	17.9	117	2	B44253	alveolar macrophag
40	83	17.9	125	2	JN0470	interferon gamma-i
41	82.5	17.8	132	2	A57325	C-X-C chemokine LI
42	82	17.7	113	2	JC7800	neutrophil activat
43	82	17.7	870	2	A41130	dystrophin homolog
44	81.5	17.6	75	2	B54188	granulocyte chemot
45	79	17.1	92	2	I46730	immune activation

ALIGNMENTS

RESULT 1
G01540
cytokine SDF-1-beta - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C;Accession: G01540
R;Spotila, L.D.
submitted to the EMBL Data Library, October 1994
A;Reference number: G07697
A;Accession: G01540
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-93 <SPO>
A;Cross-references: UNIPROT:P48061; UNIPARC:UPI000003092F; EMBL:U16752;
NID:g1272194; PID:g571508
C;Superfamily: beta-thromboglobulin

Query Match 100.0%; Score 463; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 4.2e-45;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60

Qy         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
              |||||||||||||||||||||||||||||
Db         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
```

RESULT 2
I53416
interleukin-8 homolog - mouse
C;Species: Mus sp. (mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C;Accession: I53416
R;Jiang, W.; Zhou, P.; Kahn, S.M.; Tomita, N.; Johnson, M.D.; Weinstein, I.B.
Exp. Cell Res. 215, 284-293, 1994
A;Title: Molecular cloning of TPAR1, a gene whose expression is repressed by the tumor promoter 12-O-tetradecanoylphorbol 13-acetate (TPA).
A;Reference number: I53416; MUID:95073497; PMID:7982471
A;Accession: I53416
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-89 <RES>
A;Cross-references: UNIPARC:UPI00000018A3; GB:S74318; NID:g786393;
PIDN:AAB32650.1; PID:g786394
C;Genetics:
A;Gene: TPAR1
C;Superfamily: beta-thromboglobulin

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  Query Match             95.5%;  Score 442;  DB 2;  Length 89;
  Best Local Similarity   93.3%;  Pred. No. 9.5e-43;
  Matches   83;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
              |:|||| || ||| |||:||||||||||||||||||:||||||||||||||||||||||
Db          1 MDAKVVAVLALVLAALCISDGKPVSLSYRCPCRFFESHIARANVKHLKILNTPNCALQIV 60

Qy         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
              |||||||||||||||||||||||||||||
Db         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
```

RESULT 3
A53497
pre-B-cell growth-stimulating factor precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 09-Jul-2004
C;Accession: A53497; I59582
R;Nagasawa, T.; Kikutani, H.; Kishimoto, T.
Proc. Natl. Acad. Sci. U.S.A. 91, 2305-2309, 1994
A;Title: Molecular cloning and structure of a pre-B-cell growth-stimulating factor.
A;Reference number: A53497; MUID:94181581; PMID:8134392
A;Accession: A53497
A;Status: preliminary

A;Molecule type: mRNA
A;Residues: 1-89 <NAG>
A;Cross-references: UNIPROT:P40224; UNIPARC:UPI00000018A3; GB:D21072;
NID:g413905; PIDN:BAA04648.1; PID:g468457
R;Tashiro, K.; Tada, H.; Heilker, R.; Shirozu, M.; Nakano, T.; Honjo, T.
Science 261, 600-603, 1993
A;Title: Signal sequence trap: a cloning strategy for secreted proteins and type
I membrane proteins.
A;Reference number: I59582; MUID:93342488; PMID:8342023
A;Accession: I59582
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-89 <RES>
A;Cross-references: UNIPARC:UPI00000018A3; GB:L12029; NID:g393179;
PIDN:AAA40100.1; PID:g393180
C;Genetics:
A;Gene: SDF-1-alpha
C;Superfamily: beta-thromboglobulin
C;Keywords: cytokine

  Query Match   95.5%; Score 442; DB 2; Length 89;
  Best Local Similarity   93.3%; Pred. No. 9.5e-43;
  Matches   83; Conservative   3; Mismatches   3; Indels   0; Gaps   0;

Qy   1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
              |:|||| || ||| |||:||||||||||||||||||:||||||||||||||||||||
Db   1 MDAKVVAVLALVLAALCISDGKPVSLSYRCPCRFFESHIARANVKHLKILNTPNCALQIV 60

Qy   61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
              |||||||||||||||||||||||||||||
Db   61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89

RESULT 4
I81182
cytokine - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C;Accession: I81182
R;Tashiro, K.; Tada, H.; Heilker, R.; Shirozu, M.; Nakano, T.; Honjo, T.
Science 261, 600-603, 1993
A;Title: Signal sequence trap: a cloning strategy for secreted proteins and type
I membrane proteins.
A;Reference number: I59582; MUID:93342488; PMID:8342023
A;Accession: I81182
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-93 <RES>
A;Cross-references: UNIPROT:P40224; UNIPARC:UPI000002A125; GB:L12030;
NID:g393181; PIDN:AAA40101.1; PID:g393182
C;Genetics:
A;Gene: SDF-1-beta
C;Superfamily: beta-thromboglobulin

  Query Match   95.5%; Score 442; DB 2; Length 93;
  Best Local Similarity   93.3%; Pred. No. 9.9e-43;
  Matches   83; Conservative   3; Mismatches   3; Indels   0; Gaps   0;

```
Qy          1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIV 60
              |:|||| || ||| |||:||||||||||||||||||:||||||||||||||||||||
Db          1 MDAKVVAVLALVLAALCISDGKPVSLSYRCPCRFFESHIARANVKHLKILNTPNCALQIV 60

Qy         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
              |||||||||||||||||||||||||||||
Db         61 ARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
```

RESULT 5
I48148
Neutrophil attractant protein-1 - guinea pig
C;Species: Cavia porcellus (guinea pig)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I48148
R;Yoshimura, T.; Johnson, D.G.
J. Immunol. 151, 6225-6236, 1993
A;Title: cDNA cloning and expression of guinea pig neutrophil attractant protein-1 (NAP-1): NAP-1 is highly conserved in guinea pig.
A;Reference number: I48148; MUID:94065176; PMID:7504015
A;Accession: I48148
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-101 <RES>
A;Cross-references: UNIPROT:P49113; UNIPARC:UPI000012D4F8; GB:L04986; NID:g459764; PIDN:AAA37049.1; PID:g459765
C;Genetics:
A;Gene: NAP-1
C;Superfamily: beta-thromboglobulin

  Query Match   24.5%; Score 113.5; DB 2; Length 101;
  Best Local Similarity   32.6%; Pred. No. 1.3e-05;
  Matches   30; Conservative   20; Mismatches   31; Indels   11; Gaps   6;

```
Qy          6 VVVLVLVLTALCLSDGKPVS---LSYRCPCRFFESHVARAN---VKHLKILNT-PNCA-L 57
              | ||   | :  | :|  |:      || |   : |    :   :| ||:: : | ||
Db          7 VAVLAAFLLSAVLCEGMVVTKLVSELRCQC--IKIHTTPFHPKFIKELKVIESGPRCANS 64

Qy         58 QIVARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
              :|: :| ::|||:|:||| ||:|: :   | :
Db         65 EIIVKL-SDNRQLCLDPKKKWVQDVVSMFLKR 95
```

RESULT 6
A37034
interleukin-8 precursor - human
N;Alternate names: beta-thromboglobulin-like protein; fibroblast-derived neutrophil-activating factor alpha; lung carcinoma-derived chemotaxin; lymphocyte-derived neutrophil-activating factor; monocyte-derived neutrophil chemotactic factor; monocyte-derived neutrophil-activating factor
C;Species: Homo sapiens (man)
C;Date: 08-Dec-1992 #sequence_revision 08-Dec-1992 #text_change 09-Jul-2004
C;Accession: A37034; JL0041; A32791; S37634; PL0107; A28598; A27488; A39960; A60401; A60591; S15827; S04216; A60567; A60847; S15417; S03975; I54560; I55992; I37902; S67519
R;Mukaida, N.; Shiroo, M.; Matsushima, K.

J. Immunol. 143, 1366-1371, 1989
A;Title: Genomic structure of the human monocyte-derived neutrophil chemotactic factor IL-8.
A;Reference number: A37034; MUID:89309826; PMID:2663993
A;Accession: A37034
A;Molecule type: DNA
A;Residues: 1-99 <MUK>
A;Cross-references: UNIPROT:P10145; UNIPARC:UPI0000000DD0; GB:M28130; NID:g186367; PIDN:AAA59158.1; PID:g186368
A;Note: the authors failed to translate the last thirty-six nucleotides of the second exon
R;Matsushima, K.; Morishita, K.; Yoshimura, T.; Lavu, S.; Kobayashi, Y.; Lew, W.; Appella, E.; Kung, H.F.; Leonard, E.J.; Oppenheim, J.J.
J. Exp. Med. 167, 1883-1893, 1988
A;Title: Molecular cloning of a human monocyte-derived neutrophil chemotactic factor (MDNCF) and the induction of MDNCF mRNA by interleukin 1 and tumor necrosis factor.
A;Reference number: JL0041; MUID:88258376; PMID:3260265
A;Accession: JL0041
A;Molecule type: mRNA
A;Residues: 1-99 <MA1>
A;Cross-references: UNIPARC:UPI0000000DD0; EMBL:Y00787; NID:g34518; PIDN:CAA68742.1; PID:g34519
A;Note: the sequence shows similarity to several platelet-derived factors, a v-src-induced protein, a growth-regulated gene product (gro), and an IFN-gamma-inducible protein
R;Kowalski, J.; Denhardt, D.T.
Mol. Cell. Biol. 9, 1946-1957, 1989
A;Title: Regulation of the mRNA for monocyte-derived neutrophil-activating peptide in differentiating HL60 promyelocytes.
A;Reference number: A32791; MUID:89313739; PMID:2664463
A;Accession: A32791
A;Molecule type: mRNA
A;Residues: 1-99 <KOW>
A;Cross-references: UNIPARC:UPI0000000DD0; GB:M26383; NID:g188627; PIDN:AAA36323.1; PID:g188628
R;King, C.H.; Gordon, G.S.; Konieczkowski, M.; Sedor, J.R.
submitted to the EMBL Data Library, February 1992
A;Reference number: S37634
A;Accession: S37634
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-97 <KIN>
A;Cross-references: UNIPARC:UPI000000077C; EMBL:Z11686; NID:g33958; PIDN:CAA77745.1; PID:g33959
R;Suzuki, K.; Miyasaka, H.; Ota, H.; Yamakawa, Y.; Tagawa, M.; Kuramoto, A.; Mizuno, S.
J. Exp. Med. 169, 1895-1901, 1989
A;Title: Purification and partial primary sequence of a chemotactic protein for polymorphonuclear leukocytes derived from human lung giant cell carcinoma LU65C cells.
A;Reference number: PL0107; MUID:89279141; PMID:2659722
A;Accession: PL0107
A;Molecule type: protein
A;Residues: 23-32,'XR',35,'X',37-52,'L',54 <SUZ>
A;Cross-references: UNIPARC:UPI0000177BEA
A;Experimental source: lung giant cell carcinoma LU65C

R;Gregory, H.; Young, J.; Schroeder, J.M.; Mrowietz, U.; Christophers, E.
Biochem. Biophys. Res. Commun. 151, 883-890, 1988
A;Title: Structure determination of a human lymphocyte derived neutrophil activating peptide (LYNAP).
A;Reference number: A28598; MUID:88162914; PMID:3279957
A;Accession: A28598
A;Molecule type: protein
A;Residues: 28-99 <GRE>
A;Cross-references: UNIPARC:UPI000003094C
R;Walz, A.; Peveri, P.; Aschauer, H.; Baggiolini, M.
Biochem. Biophys. Res. Commun. 149, 755-761, 1987
A;Title: Purification and amino acid sequencing of NAF, a novel neutrophil-activating factor produced by monocytes.
A;Reference number: A27488; MUID:88106502; PMID:3322281
A;Accession: A27488
A;Molecule type: protein
A;Residues: 28-59 <WAL>
A;Cross-references: UNIPARC:UPI0000177BEB
R;Yoshimura, T.; Matsushima, K.; Tanaka, S.; Robinson, E.A.; Appella, E.; Oppenheim, J.J.; Leonard, E.J.
Proc. Natl. Acad. Sci. U.S.A. 84, 9233-9237, 1987
A;Title: Purification of a human monocyte-derived neutrophil chemotactic factor that has peptide sequence similarity to other host defense cytokines.
A;Reference number: A39960; MUID:88097462; PMID:3480540
A;Accession: A39960
A;Molecule type: protein
A;Residues: 28-69 <YOS>
A;Cross-references: UNIPARC:UPI0000177BEC
R;Schroeder, J.M.; Sticherling, M.; Henneicke, H.H.; Preissner, W.C.; Christophers, E.
J. Immunol. 144, 2223-2232, 1990
A;Title: IL-1alpha or tumor necrosis factor-alpha stimulate release of three NAP-1/IL-8-related neutrophil chemotactic proteins in human dermal fibroblasts.
A;Reference number: A60401; MUID:90187866; PMID:2179408
A;Accession: A60401
A;Molecule type: protein
A;Residues: 23-32 <SCH>
A;Cross-references: UNIPARC:UPI0000158437
A;Experimental source: dermal fibroblasts
A;Note: a minor component of this material (15%) includes an additional two amino acids at the amino end
R;Van Damme, J.; Decock, B.; Conings, R.; Lenaerts, J.P.; Opdenakker, G.; Billiau, A.
Eur. J. Immunol. 19, 1189-1194, 1989
A;Title: The chemotactic activity for granulocytes produced by virally infected fibroblasts is identical to monocyte-derived interleukin 8.
A;Reference number: A60591; MUID:89338542; PMID:2668011
A;Accession: A60591
A;Molecule type: protein
A;Residues: 23-33,'X',35,'X',37-42 <VAN>
A;Cross-references: UNIPARC:UPI000006F8F7
R;Nakagawa, H.; Hatakeyama, S.; Ikesue, A.; Miyai, H.
FEBS Lett. 282, 412-414, 1991
A;Title: Generation of interleukin-8 by plasmin from AVLPR-interleukin-8, the human fibroblast-derived neutrophil chemotactic factor.
A;Reference number: S15827; MUID:91243843; PMID:1828038
A;Accession: S15827

A;Molecule type: protein
A;Residues: 23-33,'X',35,'X',37-47 <FEB>
A;Cross-references: UNIPARC:UPI000006D6FA
R;van Damme, J.; van Beeumen, J.; Conings, R.; Decock, B.; Billiau, A.
Eur. J. Biochem. 181, 337-344, 1989
A;Title: Purification of granulocyte chemotactic peptide/interleukin-8 reveals N-terminal sequence heterogeneity similar to that of beta-thromboglobulin.
A;Reference number: S04216; MUID:89231715; PMID:2523801
A;Accession: S04216
A;Molecule type: protein
A;Residues: 21-67 <VA2>
A;Cross-references: UNIPARC:UPI0000177BED
R;Yoshimura, T.; Robinson, E.A.; Appella, E.; Matsushima, K.; Showalter, S.D.; Skeel, A.; Leonard, E.J.
Mol. Immunol. 26, 87-93, 1989
A;Title: Three forms of monocyte-derived neutrophil chemotactic factor (MDNCF) distinguished by different lengths of the amino-terminal sequence.
A;Reference number: A60567; MUID:89181632; PMID:2648135
A;Accession: A60567
A;Molecule type: protein
A;Residues: 21-33,'X',35,'X',37-47 <YO2>
A;Cross-references: UNIPARC:UPI0000177BEE
A;Note: the forms starting from positions 21, 23, and 28 represented 8%, 47%, and 45%, respectively, of total interleukin-8
R;Van Damme, J.; Van Beeumen, J.; Opdenakker, G.; Billiau, A.
J. Exp. Med. 167, 1364-1376, 1988
A;Title: A novel, NH-2-terminal sequence-characterized human monokine possessing neutrophil chemotactic, skin-reactive, and granulocytosis-promoting activity.
A;Reference number: A60847; MUID:88187604; PMID:3258625
A;Accession: A60847
A;Molecule type: protein
A;Residues: 28-47 <VA3>
A;Cross-references: UNIPARC:UPI0000177BEF
R;Car, B.D.; Baggiolini, M.; Walz, A.
Biochem. J. 275, 581-584, 1991
A;Title: Formation of neutrophil-activating peptide 2 from platelet-derived connective-tissue-activating peptide III by different tissue proteinases.
A;Reference number: S15417; MUID:91248085; PMID:2039437
A;Accession: S15417
A;Status: preliminary
A;Molecule type: protein
A;Residues: 28-99 <CAR>
A;Cross-references: UNIPARC:UPI000003094C
R;Golds, E.E.; Mason, P.; Nyirkos, P.
Biochem. J. 259, 585-588, 1989
A;Title: Inflammatory cytokines induce synthesis and secretion of gro protein and a neutrophil chemotactic factor but not beta-2--microglobulin in human synovial cells and fibroblasts.
A;Reference number: S03975; MUID:89246368; PMID:2655583
A;Accession: S03975
A;Molecule type: protein
A;Residues: 23-46 <GOL>
A;Cross-references: UNIPARC:UPI0000177BF0
R;Hotta, K.; Hayashi, K.; Ishikawa, J.; Tagawa, M.; Hashimoto, K.; Mizumo, S.; Suzuki, K.
Immunol. Lett. 24, 165-170, 1990

A;Title: Coding region structure of interleukin-8 gene of human lung giant cell carcinoma LU65C cells that produce LUCT/interliukin-8: homogeneity in interleuki-8 genes.
A;Reference number: I54560; MUID:90346419; PMID:2200751
A;Accession: I54560
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-99 <RES>
A;Cross-references: UNIPARC:UPI0000000DD0; GB:D14283; NID:g219915; PIDN:BAA03245.1; PID:g219916
R;Schmid, J.; Weissmann, C.
J. Immunol. 139, 250-256, 1987
A;Title: Induction of mRNA for a serine protease and a beta-thromboglobulin-like protein in mitogen-stimulated human leukocytes.
A;Reference number: I55992; MUID:87224164; PMID:2953813
A;Accession: I55992
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-99 <RE2>
A;Cross-references: UNIPARC:UPI0000000DD0; GB:M17017; NID:g179579; PIDN:AAA35611.1; PID:g179580
R;Kusner, D.J.; Luebbers, E.L.; Nowinski, R.J.; Konieczkowski, M.; King, C.H.; Sedor, J.R.
Kidney Int. 39, 1240-1248, 1991
A;Title: Cytokine- and LPS-induced synthesis of interleukin-8 from human mesangial cells.
A;Reference number: I37902; MUID:91374977; PMID:1895676
A;Accession: I37902
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-97 <RE3>
A;Cross-references: UNIPARC:UPI000000077C; EMBL:Z11686; NID:g33958; PIDN:CAA77745.1; PID:g33959
R;Alouani, S.; Gaertner, H.F.; Mermod, J.J.; Power, C.A.; Bacon, K.B.; Wells, T.N.C.; Proudfoot, A.E.I.
Eur. J. Biochem. 227, 328-334, 1995
A;Title: A fluorescent interleukin-8 receptor probe produced by targetted labelling at the amino terminus.
A;Reference number: S67519; MUID:95154308; PMID:7851404
A;Accession: S67519
A;Molecule type: mRNA
A;Residues: 1-99 <ALO>
A;Cross-references: UNIPARC:UPI0000000DD0
C;Comment: This secretory protein is chemotactic for polymorphonuclear leukocytes.
C;Comment: This protein is variably processed at the amino end. The major form differs in different cell types.
C;Genetics:
A;Gene: GDB:IL8
A;Cross-references: GDB:120099; OMIM:146930
A;Map position: 4q13-4q21
A;Introns: 22/1; 67/2; 95/2
C;Superfamily: beta-thromboglobulin
C;Keywords: chemotaxis; cytokine; inflammation
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-99/Product: interleukin-8, minor form #status experimental <MATA>

F;23-99/Product: interleukin-8, major fibroblast-derived form #status experimental <MATB>
F;28-99/Product: interleukin-8, major lymphocyte/monocyte-derived form #status experimental <MATC>

Query Match 24.4%; Score 113; DB 2; Length 99;
Best Local Similarity 31.2%; Pred. No. 1.4e-05;
Matches 30; Conservative 23; Mismatches 35; Indels 8; Gaps 6;

```
Qy          1 MNAKVVVVLV---LVLTALCLSDGKPVSL-SYRCPC-RFFESHVARANVKHLKILNT-PN 54
              | :|: | |:   |:  |||     | |    || | : :        :| |::: : |:
Db          1 MTSKLAVALLAAFLISAALCEGAVLPRSAKELRCQCIKTYSKPFHPKFIKELRVIESGPH 60

Qy         55 CA-LQIVARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
              ||  :|: :| :: |::|:|||  |:|  :|| | :
Db         61 CANTEIIVKL-SDGRELCLDPKENWVQRVVEKFLKR 95
```

RESULT 7
A32954
gro-alpha precursor - mouse
N;Alternate names: gro protein; growth regulated protein; melanoma growth-stimulating activity factor; melanoma mitogenic protein; secretory protein N51
C;Species: Mus musculus (house mouse)
C;Date: 20-Oct-1989 #sequence_revision 20-Oct-1989 #text_change 09-Jul-2004
C;Accession: A32954; JH0081
R;Oquendo, P.; Alberta, J.; Wen, D.; Graycar, J.L.; Derynck, R.; Stiles, C.D.
J. Biol. Chem. 264, 4133-4137, 1989
A;Title: The platelet-derived growth factor-inducible KC gene encodes a secretory protein related to platelet alpha-granule proteins.
A;Reference number: A32954; MUID:89139485; PMID:2917992
A;Accession: A32954
A;Molecule type: mRNA
A;Residues: 1-96 <OQU>
A;Cross-references: UNIPROT:P12850; UNIPARC:UPI0000028840; GB:J04596; NID:g201042; PIDN:AAA40131.1; PID:g201043
R;Ryseck, R.P.; MacDonald-Bravo, H.; Mattei, M.G.; Bravo, R.
Exp. Cell Res. 180, 266-275, 1989
A;Title: Cloning and sequence of a secretory protein induced by growth factors in mouse fibroblasts.
A;Reference number: JH0081; MUID:89078502; PMID:2909392
A;Accession: JH0081
A;Molecule type: mRNA
A;Residues: 1-96 <RYS>
A;Cross-references: UNIPARC:UPI0000028840
C;Comment: This protein is basic and lacks threonine, phenylalanine, and tyrosine.
C;Genetics:
A;Map position: 5
C;Superfamily: beta-thromboglobulin
C;Keywords: extracellular protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-96/Product: gro-alpha #status predicted <MAT>

Query Match 24.3%; Score 112.5; DB 2; Length 96;
Best Local Similarity 31.2%; Pred. No. 1.6e-05;
Matches 25; Conservative 22; Mismatches 30; Indels 3; Gaps 3;

```
Qy          10 VLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKIL-NTPNCA-LQIVARLKNNN 67
               :|:|    |: | |::   || |    : :   |:: ||:| : |:|   :::| || |
Db          13 LLLLATSRLATGAPIANELRCQCLQTMAGIHLKNIQSLKVLPSGPHCTQTEVIATLK-NG 71

Qy          68 RQVCIDPKLKWIQEYLEKAL 87
               |: |:||:   :|: ::| |
Db          72 REACLDPEAPLVQKIVQKML 91
```

RESULT 8
JN0841
interleukin-8 - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 12-Apr-1995
C;Accession: JN0841
R;Ishikawa, J.; Suzuki, S.; Hotta, K.; Hirota, Y.; Mizuno, S.; Suzuki, K.
Gene 131, 305-306, 1993
A;Title: Cloning of a canine gene homologous to the human interleukin-8-encoding gene.
A;Reference number: JN0841; MUID:94010328; PMID:7916715
A;Accession: JN0841
A;Molecule type: DNA
A;Residues: 1-95 <ISH>
A;Cross-references: UNIPARC:UPI0000177BDC
C;Comment: This protein is a polymorphonuclear leukocyles chemotactic factor and is involved in the host defense function.
C;Genetics:
A;Introns: 22/1; 67/2
C;Superfamily: beta-thromboglobulin

```
  Query Match             24.0%;  Score 111;  DB 2;  Length 95;
  Best Local Similarity   33.7%;  Pred. No. 2.3e-05;
  Matches   34;  Conservative   20;  Mismatches   29;  Indels   18;  Gaps    7;

Qy           1 MNAKVVVVLV---LVLTALC----LSDGKPVSLSYRCPCRFFESHVARANVKHLKILNT- 52
               | :|: | |:   ::  |||    ||    ||   || |   ::|    : |::| |
Db           1 MTSKLAVALLAAFVLSAALCEAAVLS---RVSSELRCQC--IKTHSTPFHPKYIKELRVI 55

Qy          53 ---PNCA-LQIVARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
                   |:|   :|: :| | | :||:||| ||:|: ::  | |
Db          56 DSGPHCENSEIIVKLFNGN-EVCLDPKEKWVQKVVQIFLKK 95
```

RESULT 9
I59277
Mob-1 - rat
C;Species: Rattus sp. (rat)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Aug-1999
C;Accession: I59277
R;Liang, P.; Averboukh, L.; Zhu, W.; Pardee, A.B.
Proc. Natl. Acad. Sci. U.S.A. 91, 12515-12519, 1994
A;Title: Ras activation of genes: Mob-1 as a model.
A;Reference number: I59277; MUID:95107988; PMID:7809069
A;Accession: I59277
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA

A;Residues: 1-98 <RES>
A;Cross-references: UNIPARC:UPI0000136774; EMBL:U17035; NID:g763535;
PIDN:AAB60485.1; PID:g602432
C;Genetics:
A;Gene: mob-1
C;Superfamily: beta-thromboglobulin

  Query Match   24.0%; Score 111; DB 2; Length 98;
  Best Local Similarity   33.0%; Pred. No. 2.4e-05;
  Matches   31; Conservative   22; Mismatches   33; Indels   8; Gaps   4;

Qy   1 MNAKVVVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARAN-VKHLKI----LNTPNC 55
              || ||| ||| :| : | |:: : || | | | : |:| |: |:
Db   1 MNPSAAVVLCLVLLSLSGTQGIPLARTVRCTCIDFHEQTLRPRAIGKLEIIPASLSCPH- 59

Qy   56 ALQIVARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
               ::|:| :| || : |::|: : |: | ||:::
Db   60 -VEIIATMKKNNEKRCLNPESEAIKSLL-KAVSQ 91

RESULT 10
A26736
transformation-induced protein precursor (clone 9E3) - chicken
C;Species: Gallus gallus (chicken)
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
C;Accession: A26736
R;Sugano, S.; Stoeckle, M.Y.; Hanafusa, H.
Cell 49, 321-328, 1987
A;Title: Transformation by Rous sarcoma virus induces a novel gene with homology
to a mitogenic platelet protein.
A;Reference number: A26736; MUID:87187628; PMID:3032449
A;Accession: A26736
A;Molecule type: mRNA
A;Residues: 1-103 <SUG>
A;Cross-references: UNIPROT:P08317; UNIPARC:UPI000000031A; GB:M16199;
NID:g211735; PIDN:AAA48758.1; PID:g211736
C;Superfamily: beta-thromboglobulin
C;Keywords: growth factor
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-103/Product: transformation-induced protein #status predicted <MAT>

  Query Match   23.8%; Score 110; DB 2; Length 103;
  Best Local Similarity   32.3%; Pred. No. 3.2e-05;
  Matches   30; Conservative   23; Mismatches   32; Indels   8; Gaps   6;

Qy   1 MNAKVVVVLVLVLTALCLSDGKP-VSLSYRCPCRFFESH---VARANVKHLKIL-NTPNC 55
              || |: || |:| : || |: | : |:   :| :   ::: :|: : |:|
Db   1 MNGKLGAVLALLLVSAALSQGRTLVKMGNELRCQCISTHSKFIHPKSIQDVKLTPSGPHC 60

Qy   56 A-LQIVARLKNNNRQVCIDPKLKWIQEYLEKAL 87
                ::|:| || : |:||:|| |:| : |||
Db   61 KNVEIIATLK-DGREVCLDPTAPWVQ-LIVKAL 91

RESULT 11
I50417
RSV-induced protein - chicken

C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I50417
R;Bedard, P.
Proc. Natl. Acad. Sci. U.S.A. 84, 6715-6719, 1987
A;Title: Constitutive expression of a gene encoding a polypeptide homologous to biologically active human platelet protein in Rous sarcoma virus-transformed fibroblasts virus transformed fibroblasts.
A;Reference number: I50417; MUID:88016162; PMID:2821543
A;Accession: I50417
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-103 <BED>
A;Cross-references: UNIPROT:P08317; UNIPARC:UPI00001713A9; GB:J02975; NID:g212643; PIDN:AAA49059.1; PID:g212644
C;Superfamily: beta-thromboglobulin

  Query Match 23.3%; Score 108; DB 2; Length 103;
  Best Local Similarity 32.3%; Pred. No. 5.4e-05;
  Matches 30; Conservative 22; Mismatches 33; Indels 8; Gaps 6;

```
Qy          1 MNAKVVVVLVLVLTALCLSDGKP-VSLSYRCPCRFFESH---VARANVKHLKIL-NTPNC 55
              || |   || |:| :  || |:  | :     |:   :|   :   ::: :|:  : |:|
Db          1 MNGKFGAVLALLLVSAALSQGRTLVKMGNELRCQCISTHSKFIHPKSIQDVKLTPSGPHC 60

Qy         56 A-LQIVARLKNNNRQVCIDPKLKWIQEYLEKAL 87
                ::|:| || : |:||:||   |:|  : |||
Db         61 KNVEIIATLK-DGREVCLDPTAPWVQ-LIVKAL 91
```

RESULT 12
S42496
interleukin-8 precursor [similarity] - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S42496; I46997
R;Legastelois, I.; Greenland, T.; Arnaud, P.; Mornex, J.F.; Cordier, G.
submitted to the EMBL Data Library, March 1994
A;Description: Nucleotide sequence of ovine interleukin 8 cDNA using polymerase chain reaction.
A;Reference number: S42496
A;Accession: S42496
A;Molecule type: mRNA
A;Residues: 1-101 <LEG>
A;Cross-references: UNIPROT:P36925; UNIPARC:UPI000012D4FE; EMBL:X78306; NID:g463253; PIDN:CAA55115.1; PID:g463254
R;Seow, H.F.; Yoshimura, T.; Wood, P.R.; Colditz, I.G.
Immunol. Cell Biol. 72, 398-405, 1994
A;Title: Cloning, sequencing, expression and inflammatory activity in skin of ovine interleukin-8.
A;Reference number: I46997; MUID:95137691; PMID:7835984
A;Accession: I46997
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-101 <SEO>
A;Cross-references: UNIPARC:UPI000012D4FE; GB:S74436; NID:g786590; PIDN:AAB33241.1; PID:g786591

```
C;Genetics:
A;Gene: IL-8
C;Superfamily: beta-thromboglobulin
C;Keywords: chemotaxis; cytokine; inflammation
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-101/Product: interleukin-8 #status predicted <MAT>

  Query Match             23.1%;  Score 107;  DB 2;  Length 101;
  Best Local Similarity   30.7%;  Pred. No. 6.9e-05;
  Matches   31;  Conservative   25;  Mismatches   27;  Indels   18;  Gaps    8;

Qy          1 MNAKVVVVLV---LVLTALC----LSDGKPVSLSYRCPCRFFESHVARAN---VKHLKIL 50
              | :|: | |:   |:  |||    ||    :|   || |   ::|    :   :| |:::
Db          1 MTSKLAVALLAAFLLSAALCEAAVLS---RMSTELRCQC--IKTHSTPFHPKFIKELRVI 55

Qy         51 NT-PNCA-LQIVARLKNNNRQVCIDPKLKWIQEYLEKALNK 89
               : |:|   :|: :|  | ::||:||| ||:|: ::  | :
Db         56 ESGPHCENSEIIVKL-TNGKEVCLDPKEKWVQKVVQAFLKR 95


RESULT 13
A28815
monocyte chemoattractant cytokine RANTES precursor - human
N;Alternate names: small inducible cytokine A5; T-cell specific cytokine RANTES
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1989 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: A28815
R;Schall, T.J.; Jongstra, J.; Dyer, B.J.; Jorgensen, J.; Clayberger, C.; Davis,
M.M.; Krensky, A.M.
J. Immunol. 141, 1018-1025, 1988
A;Title: A human T cell-specific molecule is a member of a new gene family.
A;Reference number: A28815; MUID:88285659; PMID:2456327
A;Accession: A28815
A;Molecule type: mRNA
A;Residues: 1-91 <SCH>
A;Cross-references: UNIPROT:P13501; UNIPARC:UPI000004A187; GB:M21121
C;Comment: The acronym RANTES reflects the description "Regulated upon
Activation, Normal T Expressed, Secreted".
C;Genetics:
A;Gene: GDB:SCYA5; D17S136E
A;Cross-references: GDB:120749; OMIM:187011
A;Map position: 17q11.2-17q12
C;Superfamily: macrophage inflammatory protein
C;Keywords: chemotaxis; cytokine; immediate-early protein; inflammation; T-cell
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-91/Product: T-cell protein RANTES #status predicted <MAT>

  Query Match             23.0%;  Score 106.5;  DB 1;  Length 91;
  Best Local Similarity   33.3%;  Pred. No. 7.1e-05;
  Matches   27;  Conservative   18;  Mismatches   29;  Indels    7;  Gaps    5;

Qy          7 VVLVLVLTALCL-SDGKPVSLSYRCPCRFFESHVARANVK-HLK--ILNTPNCALQIVAR 62
              : ::|: ||||  :   | | |   || |  :::||   : |:|     :  |:   |
Db          8 LAVILIATALCAPASASPYS-SDTTPCCF--AYIARPLPRAHIKEYFYTSGKCSNPAVVF 64

Qy         63 LKNNNRQVCIDPKLKWIQEYL 83
              :   ||||| :|: ||::||:
```

Db 65 VTRKNRQVCANPEKKWVREYI 85

RESULT 14
A46539
monocyte chemoattractant cytokine RANTES precursor - mouse
N;Alternate names: MuRantes
C;Species: Mus musculus (house mouse)
C;Date: 18-Jun-1993 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: I48875; A46539; I48654; I56970
R;Danoff, T.M.; Lalley, P.A.; Chang, Y.S.; Heeger, P.S.; Neilson, E.G.
J. Immunol. 152, 1182-1189, 1994
A;Title: Cloning, genomic organization, and chromosomal localization of the Scya5 gene encoding the murine chemokine RANTES.
A;Reference number: I48875; MUID:94132613; PMID:7507961
A;Accession: I48875
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-91 <DAN>
A;Cross-references: UNIPROT:P30882; UNIPARC:UPI000000028C; EMBL:U02298; NID:g460090; PIDN:AAA18302.1; PID:g460091
R;Schall, T.J.; Simpson, N.J.; Mak, J.Y.
Eur. J. Immunol. 22, 1477-1481, 1992
A;Title: Molecular cloning and expression of the murine RANTES cytokine: structural and functional conservation between mouse and man.
A;Reference number: A46539; MUID:92289805; PMID:1376260
A;Accession: A46539
A;Molecule type: mRNA
A;Residues: 1-18,'A',20-91 <SCH>
A;Cross-references: UNIPARC:UPI0000151811; GB:S37648; NID:g250207; PIDN:AAB22330.1; PID:g250208
A;Experimental source: macrophage cell line PU5-1.8
A;Note: sequence extracted from NCBI backbone (NCBIN:106768, NCBIP:106770)
R;Shin, H.S.; Drysdale, B.E.; Shin, M.L.; Noble, P.W.; Fisher, S.N.; Paznekas, W.A.
Mol. Cell. Biol. 14, 2914-2925, 1994
A;Title: Definition of a lipopolysaccharide-responsive element in the 5'-flanking regions of MuRantes and crg-2.
A;Reference number: I48654; MUID:94217689; PMID:7513046
A;Accession: I48654
A;Status: translation not shown; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-91 <SHI>
A;Cross-references: UNIPARC:UPI000000028C; EMBL:X70675; NID:g475205; PIDN:CAA50011.1; PID:g475206
R;Neilson, E.G.; Krensky, A.
Kidney Int. 41, 220-225, 1992
A;Title: Isolation and characterization of cDNA from renal tubular epithelium encoding murine Rantes: A small intercrine from the Scy superfamily.
A;Reference number: I56970; MUID:92277990; PMID:1375672
A;Accession: I56970
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-40,'E',42-91 <NEI>
A;Cross-references: UNIPARC:UPI000016380F; GB:M77747; NID:g200649; PIDN:AAA40029.1; PID:g200650

C;Comment: This chemoattractant for monocytes but not neutrophils is an immediate-early response protein to LPS stimulation.
C;Genetics:
A;Introns: 26/1; 63/2
C;Superfamily: macrophage inflammatory protein
C;Keywords: chemotaxis; cytokine; immediate-early protein; inflammation
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-91/Product: monocyte chemoattractant cytokine RANTES #status predicted <MAT>

Query Match 23.0%; Score 106.5; DB 1; Length 91;
Best Local Similarity 36.7%; Pred. No. 7.1e-05;
Matches 29; Conservative 11; Mismatches 34; Indels 5; Gaps 3;

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Qy          9 LVLVLTALCLSDGKPVSL--SYRCPCRFFESHVA--RANVKHLKILNTPNCALQIVARLK 64
              | ::|||  |    | |   |   || |    :|  ||:||      :  |:   |  :
Db          8 LTIILTAAALCTPAPASPYGSDTTPCCFAYLSLALPRAHVKEY-FYTSSKCSNLAVVFVT 66

Qy         65 NNNRQVCIDPKLKWIQEYL 83
                |||||  :|: ||:|||:
Db         67 RRNRQVCANPEKKWVQEYI 85
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RESULT 15
B28414
growth-regulated protein precursor - Chinese hamster
C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Accession: B28414
R;Anisowicz, A.; Bardwell, L.; Sager, R.
Proc. Natl. Acad. Sci. U.S.A. 84, 7188-7192, 1987
A;Title: Constitutive overexpression of a growth-regulated gene in transformed Chinese hamster and human cells.
A;Reference number: A94184; MUID:88041072; PMID:2890161
A;Accession: B28414
A;Molecule type: mRNA
A;Residues: 1-101 <ANI>
A;Cross-references: UNIPROT:P09340; UNIPARC:UPI000012BAF7; GB:J03560; NID:g191088; PIDN:AAA36985.1; PID:g304509
A;Note: the authors translated the codon CAG for residue 52 as Glu
C;Superfamily: beta-thromboglobulin
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-101/Product: growth-regulated protein #status predicted <MAT>

Query Match 23.0%; Score 106.5; DB 2; Length 101;
Best Local Similarity 29.8%; Pred. No. 7.8e-05;
Matches 25; Conservative 24; Mismatches 32; Indels 3; Gaps 3;

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Qy          6 VVVLVLVLTALCLSDGKPVSLSYRCPCRFFESHVARANVKHLKILNT-PNCA-LQIVARL 63
              :::|:|:|    |: | ||:   || |    : |   |:: ||:    |:|   :::| |
Db         13 LLLLLLLLATSRLATGAPVANELRCQCLQTMTGVHLKNIQSLKVTPPGPHCTQTEVIATL 72

Qy         64 KNNNRQVCIDPKLKWIQEYLEKAL 87
              | | :: |::|:   :|: ::| |
Db         73 K-NGQEACLNPEAPMVQKIVQKML 95
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Search completed: April 26, 2006, 02:38:13
Job time : 39 secs